GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 17:13:55 ; Search time 572 Seconds
(without alignments)
10547.119 Million cell updates/sec

Title: US-10-614-524-1
Perfect score: 3687
Sequence: 1 ttgacttcaaataggaaaaa.....tactccttatggaggaatag 3687

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3666.2	99.4	4173	4	US-09-661-322A-37	Sequence 37, Appl
2	3266.6	88.6	3684	1	US-08-448-170-7	Sequence 7, Appli
3	3266.6	88.6	3684	3	US-08-961-803-5	Sequence 5, Appli
4	3260.2	88.4	3684	4	US-09-661-322A-62	Sequence 62, Appl
5	3133.6	85.0	4074	1	US-08-377-690-1	Sequence 1, Appli
6	2687.2	72.9	3934	1	US-08-100-709-3	Sequence 3, Appli
7	2687.2	72.9	3934	1	US-08-176-865-3	Sequence 3, Appli
8	2687.2	72.9	3934	1	US-08-474-038-3	Sequence 3, Appli
9	2687.2	72.9	3934	2	US-08-779-046-3	Sequence 3, Appli
10	2687.2	72.9	3934	2	US-08-881-340-3	Sequence 3, Appli
11	1793.4	48.6	3522	1	US-08-040-751-4	Sequence 4, Appli
12	1793.4	48.6	3522	1	US-08-291-368-1	Sequence 1, Appli
13	1793.4	48.6	3522	2	US-08-962-190-1	Sequence 1, Appli
14	1793.4	48.6	3522	5	PCT-US95-10310-1	Sequence 1, Appli
15	1791.8	48.6	3522	6	5164180-3	Patent No. 5164180
16	1791.8	48.6	3522	6	5164180-3	Patent No. 5164180
17	1662	45.1	4106	1	US-08-434-823-1	Sequence 1, Appli
18	1662	45.1	4106	1	US-08-457-366-1	Sequence 1, Appli
19	1581.6	42.9	3558	3	US-09-178-252-22	Sequence 22, Appl
20	1581.6	42.9	3558	4	US-09-826-660-22	Sequence 22, Appl
21	1501	40.7	3766	1	US-08-032-364-1	Sequence 1, Appli
22	1495.6	40.6	3624	1	US-07-951-715A-6	Sequence 6, Appli
23	1495.6	40.6	3624	2	US-08-459-448A-6	Sequence 6, Appli
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36	1411.4	38.3	4020	5	PCT-US91-02560-1	Sequence 1, Appli
37	1408.4	38.2	3522	1	US-07-828-788A-9	Sequence 9, Appli
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44	1408.4	38.2	3522	3	US-09-178-252-5	Sequence 5, Appli
45	1408.4	38.2	3522	4	US-09-521-344-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-661-322A-37
; Sequence 37, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 4173
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3687)
US-09-661-322A-37

Query Match 99.4%; Score 3666.2; DB 4; Length 4173;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3674; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Db       3301 AACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTATCCAACGGAT 3360

Qy       3361 ACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGTATGTAATTCCCGTAAT 3420
             |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       3361 ACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGCATGTAATTCCCGTAAT 3420

Qy       3421 GCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTACAAACCGACT 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTACAAACCGACT 3480

Qy       3481 TATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGTGAATATGACAGAGGG 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 TATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGTGAATATGACAGAGGG 3540

Qy       3541 TATGTGAATTATCCACCACTACCAGCTGGTTATATGACAAAAGAATTAGAATACTTCCCA 3600
             |||||||||||||||||||||||||||||| ||||||| |||||||||||| ||||||
Db       3541 TATGTGAATTATCCACCACTACCAGCTGGTTATGTGACAAAGGAATTAGAATATTTCCCA 3600

Qy       3601 GAAACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGGGAAGTTTATTGTAGACAGC 3660
             |||||||||||||||||||||||||||||||||||||||||||||||| |  || || || ||||||
Db       3601 GAAACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGGAACATTCATCGTGGACAGC 3660

Qy       3661 GTGGAATTACTCCTTATGGAGGAATAG 3687
                | |||||||||||||||| ||||||
Db       3661 ATAGAATTACTCCTTATGGAAGAATAG 3687
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RESULT 2
US-08-448-170-7
; Sequence 7, Application US/08448170
; Patent No. 5723758
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-448-170-7

Query Match 88.6%; Score 3266.6; DB 1; Length 3684;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 3449; Conservative 0; Mismatches 229; Indels 15; Gaps 3;

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Qy          1 TTGACTTCAAATAGGAAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAGCTGTA 60
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Db          1 TTGACTTCAAATAGGAAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAGCTGTA 60

Qy         61 TCGAATCATTCCACACAAATGGATCTATCACCAGATGCTCGTATTGAGGATTCTTTGTGT 120
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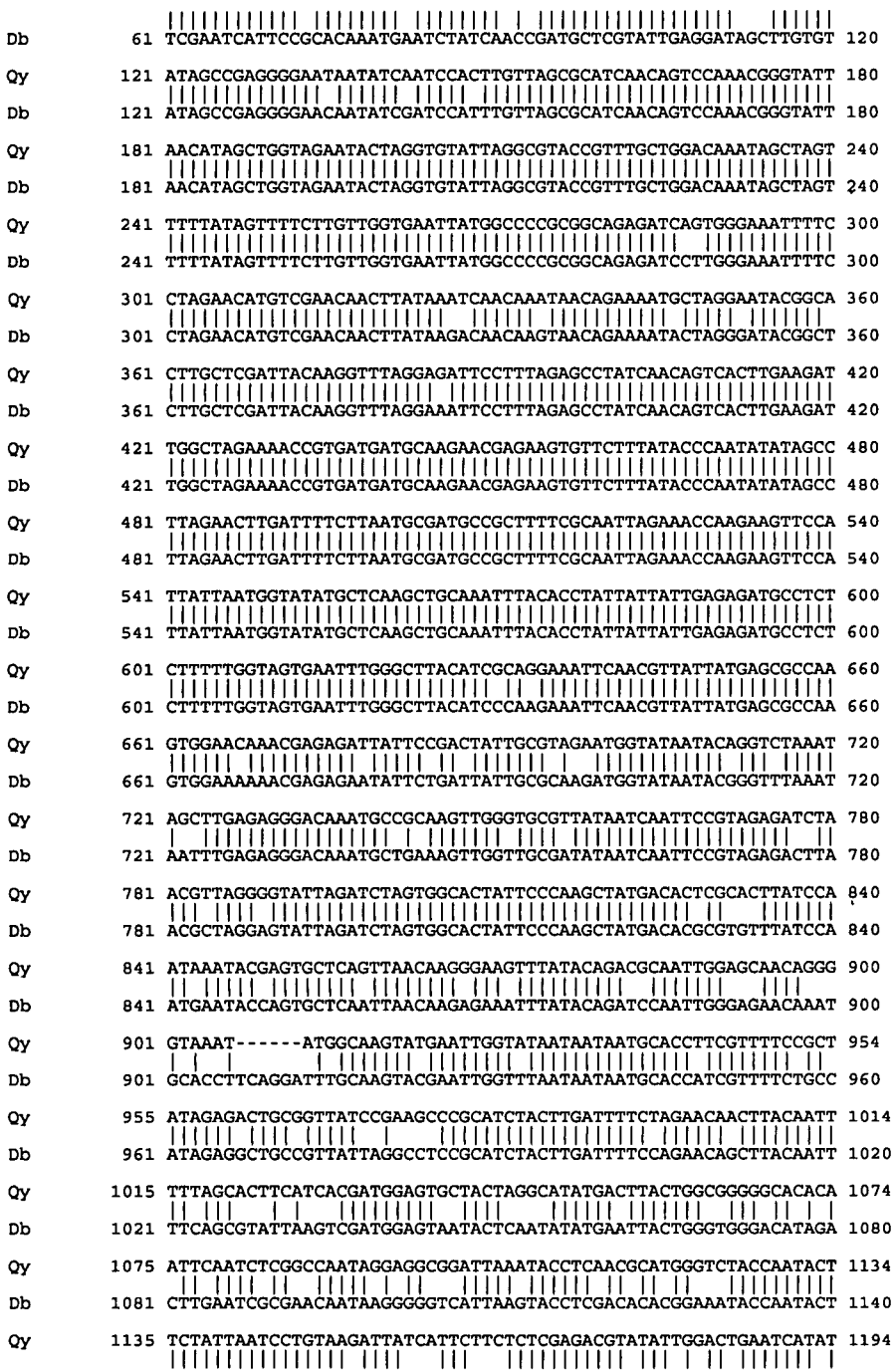
Db 61 TCGAATCATTCCGCACAAATGAATCTATCAACCGATGCTCGTATTGAGGATAGCTTGTGT 120
Qy 121 ATAGCCGAGGGGAATAATATCAATCCACTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
Db 121 ATAGCCGAGGGGAACAATATCGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
Qy 181 AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGT 240
Db 181 AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGT 240
Qy 241 TTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTC 300
Db 241 TTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCCTTGGGAAATTTTC 300
Qy 301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCA 360
Db 301 CTAGAACATGTCGAACAACTTATAAGACAACAAGTAACAGAAAATACTAGGGATACGGCT 360
Qy 361 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
Db 361 CTTGCTCGATTACAAGGTTTAGGAAATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
Qy 421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGCC 480
Db 421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGCC 480
Qy 481 TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA 540
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Qy 541 TTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATTGAGAGATGCCTCT 600
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Qy 601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTATTATGAGCGCCAA 660
Db 601 CTTTTTGGTAGTGAATTTGGGCTTACATCCCAAGAAATTCAACGTTATTATGAGCGCCAA 660
Qy 661 GTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT 720
Db 661 GTGGAAAAAACGAGAGAATATTCTGATTATTGCGCAAGATGGTATAATACGGGTTTAAAT 720
Qy 721 AGCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCAATTCCGTAGAGATCTA 780
Db 721 AATTTGAGAGGGACAAATGCTGAAAGTTGGTTGCGATATAATCAATTCCGTAGAGACTTA 780
Qy 781 ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840
Db 781 ACGCTAGGAGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACGCGTGTTTATCCA 840
Qy 841 ATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGCAATTGGAGCAACAGGG 900
Db 841 ATGAATACCAGTGCTCAATTAACAAGAGAAATTTATACAGATCCAATTGGGAGAACAAAT 900
Qy 901 GTAAAT------ATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTTTCCGCT 954
Db 901 GCACCTTCAGGATTTGCAAGTACGAATTGGTTTAATAATAATGCACCATCGTTTTCTGCC 960
Qy 955 ATAGAGACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACAACTTACAATT 1014
Db 961 ATAGAGGCTGCCGTTATTAGGCCTCCGCATCTACTTGATTTTCCAGAACAGCTTACAATT 1020
Qy 1015 TTTAGCACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGGCGGGGGCACACA 1074
Db 1021 TTCAGCGTATTAAGTCGATGGAGTAATACTCAATATATGAATTACTGGGTGGGACATAGA 1080
Qy 1075 ATTCAATCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGTCTACCAATACT 1134
Db 1081 CTTGAATCGCGAACAATAAGGGGGTCATTAAGTACCTCGACACACGGAAATACCAATACT 1140
Qy 1135 TCTATTAATCCTGTAAGATTATCATTCTTCTCTCGAGACGTATATTGGACTGAATCATAT 1194
Db 1141 TCTATTAATCCTGTAACATTACAGTTCACATCTCGAGACGTTTATAGAACAGAATCATTT 1200
Qy 1195 GCAGGAGTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCCTACTGTTAGA 1254
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Qy 1255 TTTAATTTTAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGTCAACCC 1314
Db 1255 TTTAATTGGAGAAATCCCCTGAATTCTCTT---AGAGGTAGCCTTCTCTATACTATAGGG 1311
Qy 1315 TATGAGTCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACCAGAAACAACA 1374
Db 1312 TATACTGGAGTGGGGACACAACTATTTGATTCAGAAACTGAATTACCACCAGAAACAACA 1371
Qy 1375 GAACGACCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCTCATTTCACAA 1434
Db 1372 GAACGACCAAATTATGAATCTTACAGTCATAGATTATCTAATATAAGACTAATATCAGGA 1431
Qy 1435 TCTAGGGTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGATCGTACAAATACC 1494
Db 1432 AACACTTTGAGAGCACCAGTATATTCTTGGACGCACCGTAGTGCAGATCGTACAAATACC 1491
Qy 1495 ATTAGTTCAGATAGCATAACACAAATACCATTGGTAAAATCATTCAACCTTAATTCAGGT 1554
Db 1492 ATTAGTTCAGATAGCATAACACAAATACCATTGGTAAAATCATTCAACCTTAATTCAGGT 1551
Qy 1555 ACCTCTGTAGTCAGTGGCCCAGGATTTACAGGAGGGGATATAATCCGAACTAACGTTAAT 1614
Db 1552 ACCTCTGTAGTCAGTGGCCCAGGATTTACAGGAGGGGATATAATCCGAACTAACGTTAAT 1611
Qy 1615 GGTAGTGTACTAAGTATGGGTCTTAATTTTAATAATACATCATTACAGCGGTATCGCGTG 1674
Db 1612 GGTAGTGTACTAAGTATGGGTCTTAATTTTAATAATACATCATTACAGCGGTATCGCGTG 1671
Qy 1675 AGAGTTCGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGTCGGAGGGAGTACT 1734
Db 1672 AGAGTTCGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGTCGGAGGGAGTACT 1731
Qy 1735 ACTTTTGATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAATCA 1794
Db 1732 ACTTTTGATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAATCA 1791
Qy 1795 TTTAGATTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1854
Db 1792 TTTAGATTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1851
Qy 1855 AGTATAAGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATTGAATTCATTCCA 1914
Db 1852 AGTATAAGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATTGAATTCATTCCA 1911
Qy 1915 ATTACTGCAACCTTCGAAGCAGAATACGATTTAGAAAGGGCGCAAGAGGCGGTGAATGCT 1974
Db 1912 ATTACTGCAACCTTCGAAGCAGAATATGATTTAGAAAGAGCGCAAGAGGCGGTGAATGCT 1971
Qy 1975 CTGTTTACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATTGAT 2034
Db 1972 CTGTTTACTAATACGAATCCAAGAAGGTTGAAAACAGGTGTGACAGATTATCATATTGAT 2031
Qy 2035 CAAGTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAAGAGAGAA 2094
Db 2032 GAAGTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTGGATGAAAAGAGAGAA 2091
Qy 2095 TTACTTGAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAACTTACTCCAAGAT 2154
Db 2092 TTACTTGAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAACTTACTCCAAGAT 2151
Qy 2155 CCAAACTTCACATCCATCAATAAGCAACCAGACTTCATATCTACTAATGAGCAATCGAAT 2214
Db 2152 CCAAACTTCACATCCATCAATAAGCAACCAGACTTCATATCTACTAATGAGCAATCGAAT 2211
Qy 2215 TTCACATCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTACAATC 2274
Db 2212 TTCACATCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTACAATC 2271

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Qy       2275 CAGGAAGGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGACTTTTAATGAG 2334
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Db       2272 CAGGAAGGAAATGACGTATTTAAAGAGAATTACGTCATACTACCGGGTACTTTTAATGAG 2331

Qy       2335 TGTTATCCGACGTATTTATATCAAAAAATAGGAGAGTCGGAATTAAAAGCTTATACTCGC 2394
             |||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||
Db       2332 TGTTATCCGACGTATTTATATCAAAAAATAGGGGAGGCGGAATTAAAAGCTTATACTCGC 2391

Qy       2395 TACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAT 2454
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Db       2392 TACCAATTAAGTGGCTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAC 2451

Qy       2455 AATGCGAAACATGAAACATTGGATGTTCCAGGTACCGAGTCCGTATGGCCGCTTTCAGTT 2514
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Db       2512 GAAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTTTGAATGGAAT 2571

Qy       2575 CCTGATCTAGATTGTTCCTGCAGAGATGGAGAAAAATGTGCGCATCATTCCCATCATTTC 2634
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Db       2692 TTCAAGATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAACCTGGAATTTATTGAAGAG 2751

Qy       2755 AAACCATTATTAGGAGAAGCACTGTCTCGTGTGAAGAGAGCAGAGAAAAAATGGAGAGAC 2814
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Db       2752 AAACCATTATTAGGAGAAGCACTGTCTCGTGTGAAGAGAGCAGAGAAAAAATGGAGAGAC 2811

Qy       2815 AAACGTGAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAGAAGCTGTG 2874
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Qy       2875 GATGCTTTATTTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTGGCATG 2934
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Db       2872 GATGCTTTATTTGTAGATTCTCAATATGATAGATTACAAGCGGATACAAACATTGGCATG 2931

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Db       2932 ATTCATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCGTATCTTTCAGAATTATCT 2991

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Db       2992 GTTATCCCAGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCGCATTATCACTGCA 3051

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Db       3112 TGCTGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCCTTGTT 3171

Qy       3175 ATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGCTAT 3234
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Db       3232 ATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGTTGTGTAACGATCCATGAA 3291

Qy       3295 ATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTATCCA 3354
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Db       3292 ATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTATCCA 3351

Qy       3355 ACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGTATGTAATTCC 3414
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Db       3352 ACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGCATGTAATTCC 3411

Qy       3415 CGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTACAAA 3474
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Db       3412 CGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTACAAA 3471

Qy       3475 CCGACTTATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGTGAATATGAC 3534
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Qy       3535 AGAGGGTATGTGAATTATCCACCACTACCAGCTGGTTATATGACAAAAGAATTAGAATAC 3594
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Db       3532 AGAGGGTATGTGAATTATCCACCAGTACCAGCTGGTTATATGACAAAAGAATTAGAATAC 3591

Qy       3595 TTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGGGAAGTTTATTGTA 3654
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Db       3592 TTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGGGAAGTTTATTGTA 3651

Qy       3655 GACAGCGTGGAATTACTCCTTATGGAGGAATAG 3687
             |||||||||||||||||||||||||||||||||
Db       3652 GACAGCGTGGAATTACTCCTTATGGAGGAATAG 3684
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RESULT 3
US-08-961-803-5
; Sequence 5, Application US/08961803
; Patent No. 6150589
;  GENERAL INFORMATION:
;    APPLICANT:  Payne, Jewel
;    APPLICANT:  Cummings, David A.
;    APPLICANT:  Cannon, Raymond J.C.
;    APPLICANT:  Narva, Kenneth E.
;    APPLICANT:  Stelman, Steve
;    TITLE OF INVENTION:  No. 6150589el Bacillus thuringiensis Isolate Denoted
;    TITLE OF INVENTION:  B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
;    TITLE OF INVENTION:  Encoding Lepidopteran-Active Toxins
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jay M. Sanders
;      STREET:  2421 N.W. 41st Street, Suite A-1
;      CITY:  Gainesville
;      STATE:  Florida
;      COUNTRY:  USA
;      ZIP:  32606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/961,803
;      FILING DATE:  31-OCT-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/069,902
;      FILING DATE:  01-JUNE-1993
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/759,247
;      FILING DATE:  13-SEPT-1991
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/448,170
;      FILING DATE:  23-MAY-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sanders, Jay M.
;      REGISTRATION NUMBER:  39,355
;      REFERENCE/DOCKET NUMBER:  M/S 102DCD1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (352) 375-8100
```

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;      TELEFAX:  (352) 372-5800
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3684 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-961-803-5

  Query Match             88.6%;  Score 3266.6;  DB 3;  Length 3684;
  Best Local Similarity   93.4%;  Pred. No. 0;
  Matches 3449;  Conservative    0;  Mismatches  229;  Indels   15;  Gaps    3;

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Db          1 TTGACTTCAAATAGGAAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAGCTGTA 60

Qy         61 TCGAATCATTCCACACAAATGGATCTATCACCAGATGCTCGTATTGAGGATTCTTTGTGT 120
              |||||||||||| |||||||| |||||||| | ||||||||||||||||||   ||||||
Db         61 TCGAATCATTCCGCACAAATGAATCTATCAACCGATGCTCGTATTGAGGATAGCTTGTGT 120

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              |||||||||||||| |||||| ||||| ||||||||||||||||||||||||||||||||
Db        121 ATAGCCGAGGGGAACAATATCGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180

Qy        181 AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGT 240

Qy        241 TTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTC 300
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Qy        301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCA 360
              ||||||||||||||||||||||||  |||||| |||||||||| ||||| |||||||
Db        301 CTAGAACATGTCGAACAACTTATAAGACAACAAGTAACAGAAAATACTAGGGATACGGCT 360

Qy        361 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
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Qy        421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGCC 480
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Qy        601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTATTATGAGCGCCAA 660
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Db        661 GTGGAAAAAACGAGAGAATATTCTGATTATTGCGCAAGATGGTATAATACGGGTTTAAAT 720

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Qy        841 ATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGCAATTGGAGCAACAGGG 900
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Qy       1015 TTTAGCACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGGCGGGGGCACACA 1074
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Db       1021 TTCAGCGTATTAAGTCGATGGAGTAATACTCAATATATGAATTACTGGGTGGGACATAGA 1080

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Qy       1195 GCAGGAGTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCCTACTGTTAGA 1254
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Db       1201 GCAGGGATAAATAT------ACTTCTAACTACTCCTGTGAATGGAGTACCTTGGGCTAGA 1254

Qy       1255 TTTAATTTTAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGTCAACCC 1314
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Db       1255 TTTAATTGGAGAAATCCCCTGAATTCTCTT---AGAGGTAGCCTTCTCTATACTATAGGG 1311

Qy       1315 TATGAGTCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACCAGAAACAACA 1374
              |||     |   |||   ||| ||  ||||||||||||||||||||||||||||||||
Db       1312 TATACTGGAGTGGGGACACAACTATTTGATTCAGAAACTGAATTACCACCAGAAACAACA 1371

Qy       1375 GAACGACCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCTCATTTCACAA 1434
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Db       1372 GAACGACCAAATTATGAATCTTACAGTCATAGATTATCTAATATAAGACTAATATCAGGA 1431

Qy       1435 TCTAGGGTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGATCGTACAAATACC 1494
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Db       1432 AACACTTTGAGAGCACCAGTATATTCTTGGACGCACCGTAGTGCAGATCGTACAAATACC 1491

Qy       1495 ATTAGTTCAGATAGCATAACACAAATACCATTGGTAAAATCATTCAACCTTAATTCAGGT 1554
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Qy       1795 TTTAGATTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1854
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Qy       1855 AGTATAAGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATTGAATTCATTCCA 1914
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              |||||||||||||||||||||||| |||||||||| ||||||||||||||||||||||
Db       1912 ATTACTGCAACCTTCGAAGCAGAATATGATTTAGAAAGAGCGCAAGAGGCGGTGAATGCT 1971
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Qy       1975 CTGTTTACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATTGAT 2034
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Qy       2215 TTCACATCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTACAATC 2274
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Db       2212 TTCACATCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTACAATC 2271

Qy       2275 CAGGAAGGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGACTTTTAATGAG 2334
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Qy       2395 TACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAT 2454
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RESULT 4
US-09-661-322A-62
; Sequence 62, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 62
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-661-322A-62

Query Match 88.4%; Score 3260.2; DB 4; Length 3684;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 3445; Conservative 0; Mismatches 233; Indels 15; Gaps 3;

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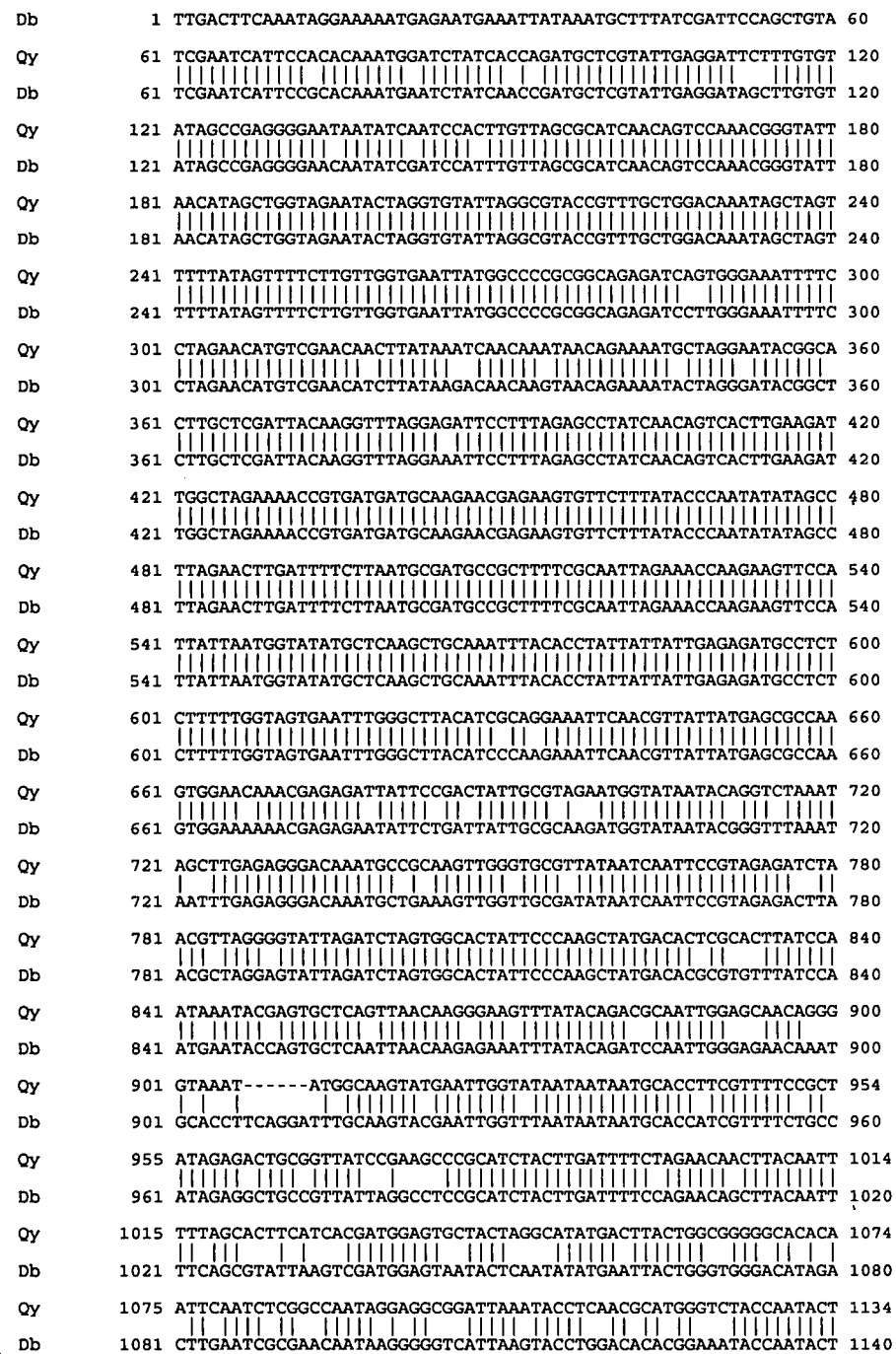

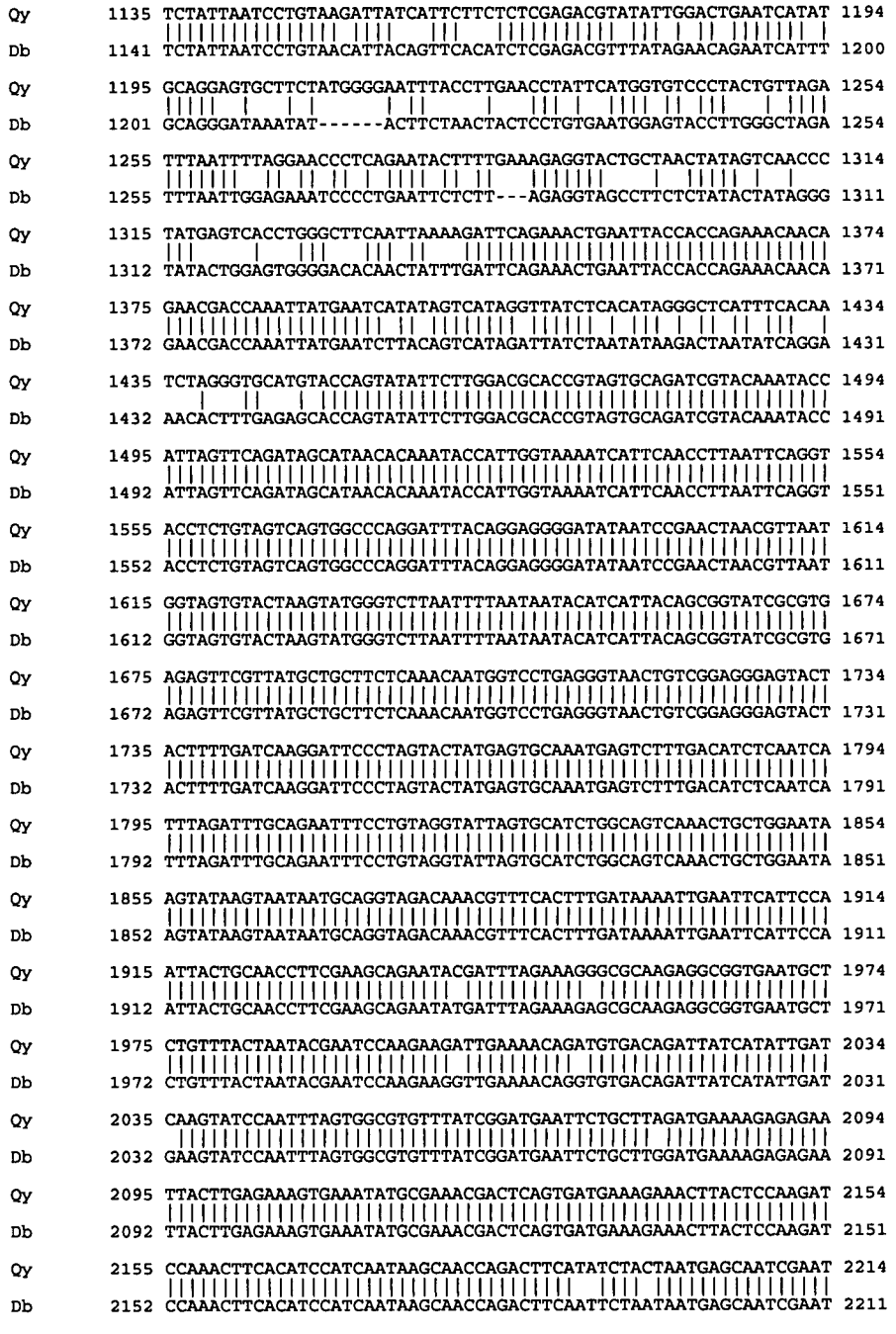

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Qy       3115 TGCTGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCCTTGTT 3174
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3112 TGCTGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCCTTGTT 3171

Qy       3175 ATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGCTAT 3234
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3172 ATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGCTAT 3231

Qy       3235 ATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGTTGTGTAACGATCCATGAA 3294
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       3232 ATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGTTGTGTAACTATCCATGAA 3291

Qy       3295 ATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTATCCA 3354
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3292 ATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTATCCA 3351

Qy       3355 ACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGTATGTAATTCC 3414
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3352 ACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGTATGTAATTCC 3411

Qy       3415 CGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTACAAA 3474
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3412 CGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTACAAA 3471

Qy       3475 CCGACTTATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGTGAATATGAC 3534
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3472 CCGACTTATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGTGAATATGAC 3531

Qy       3535 AGAGGGTATGTGAATTATCCACCACTACCAGCTGGTTATATGACAAAAGAATTAGAATAC 3594
             |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       3532 AGAGGGTATGTGAATTATCCACCAGTACCAGCTGGTTATATGACAAAAGAATTAGAATAC 3591

Qy       3595 TTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGGGAAGTTTATTGTA 3654
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3592 TTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGGGAAGTTTATTGTA 3651

Qy       3655 GACAGCGTGGAATTACTCCTTATGGAGGAATAG 3687
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Db       3652 GACAGCGTGGAATTACTCCTTATGGAGGAATAG 3684
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RESULT 5
US-08-377-690-1
; Sequence 1, Application US/08377690
; Patent No. 5628995
;  GENERAL INFORMATION:
;    APPLICANT:  PEFEROEN, Marnix
;    APPLICANT:  JANSENS, Stefan
;    APPLICANT:  DENOLF, Peter
;    TITLE OF INVENTION:  CONTROL OF OSTRINIA
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  The George Mason Bldg., Washington & Prince
;      STREET:  Sts.
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/377,690
;      FILING DATE:
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/164,781
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/938,362
;      FILING DATE:  31-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Crane-Feury, Sharon E
;      REGISTRATION NUMBER:  36,113
;      REFERENCE/DOCKET NUMBER:  010830-039
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4074 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  Bacillus thuringiensis
;      STRAIN:  entomocidus HD 110
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  186..3872
;      OTHER INFORMATION:  /note= "PROPERTIES:  CryIB is toxic to
;      OTHER INFORMATION:  Ostrinea nubilalis (among others)"
US-08-377-690-1

  Query Match             85.0%;  Score 3133.6;  DB 1;  Length 4074;
  Best Local Similarity   91.1%;  Pred. No. 0;
  Matches 3373;  Conservative    0;  Mismatches  299;  Indels   30;  Gaps    3;

Qy          1 TTGACTTCAAATAGGAAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAGCTGTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 TTGACTTCAAATAGGAAAAATGAGAATGAAATTATAAAT----------------GCTGTA 230

Qy         61 TCGAATCATTCCACACAAATGGATCTATCACCAGATGCTCGTATTGAGGATTCTTTGTGT 120
              ||||||||||||| ||||||||||||||| ||||||||||||||||||||||    ||||||
Db        231 TCGAATCATTCCGCACAAATGGATCTATTACCAGATGCTCGTATTGAGGATAGCTTGTGT 290

Qy        121 ATAGCCGAGGGGAATAATATCAATCCACTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
              ||||||||||||||| |||||  ||||| ||||||||||||||||||||||||||||||||
Db        291 ATAGCCGAGGGGAACAATATTGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATT 350

Qy        181 AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGT 240
              |||||||||||||||||||| ||||| |||||||||||||||||||| ||||||||
Db        351 AACATAGCTGGTAGAATACTAGGCGTATTGGGCGTACCGTTTGCTGGACAACTAGCTAGT 410

Qy        241 TTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 TTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTC 470

Qy        301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCT 530

Qy        361 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        531 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTCAGAGCCTATCAACAGTCACTTGAAGAT 590

Qy        421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGCC 480
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        591 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTCATACCCAATATATAGCT 650

Qy        481 TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA 710

Qy        541 TTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATTGAGAGATGCCTCT 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 TTATTGATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATTGAGAGATGCCTCT 770

Qy        601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTATTATGAGCGCCAA 660
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        771 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGCTATTATGAGCGCCAA 830

Qy        661 GTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        831 GTGGAACGAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT 890

Qy        721 AGCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCAATTCCGTAGAGATCTA 780
              |||||||||||||||||||||||||||||| || ||||||||||||||||||||||||||
Db        891 AGCTTGAGAGGGACAAATGCCGCAAGTTGGGTACGGTATAATCAATTCCGTAGAGATCTA 950

Qy        781 ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        951 ACGTTAGGAGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 1010

Qy        841 ATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGCAATTGGAGCAACAGGG 900
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||

Db       1011 ATAAATACGAGTGCTCAGTTAACAAGAGAAGTTTATACAGACGCAATTGGAGCAACAGGG 1070

Qy        901 GTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTTTCCGCTATAGAG 960
              |||||||||||||||||||||||||||||||||||||||||||||||| || || ||||||
Db       1071 GTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTCTCTGCCATAGAG 1130

Qy        961 ACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACAACTTACAATTTTTAGC 1020
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1131 GCTGCGGCTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACAACTTACAATTTTTAGC 1190

Qy       1021 ACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGGCGGGGGCACACAATTCAA 1080
              |||||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db       1191 GCTTCATCACGATGGAGTAATACTAGGCATATGACTTATTGGCGGGGGCACACGATTCAA 1250

Qy       1081 TCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGTCTACCAATACTTCTATT 1140
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1251 TCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGGCTACCAATACTTCTATT 1310

Qy       1141 AATCCTGTAAGATTATCATTCTTCTCTCGAGACGTATATTGGACTGAATCATATGCAGGA 1200
              |||||||||| ||||   |||  |||||||||| ||| ||||||||||||||||||||
Db       1311 AATCCTGTAACATTACGGTTCGCATCTCGAGACGTTTATAGGACTGAATCATATGCAGGA 1370

Qy       1201 GTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCCTACTGTTAGATTTAAT 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1371 GTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCCTACTGTTAGGTTTAAT 1430

Qy       1261 TTTAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGTCAACCCTATGAG 1320
              |||| |||||||||||||| || ||| |||||||| ||||||||||||||||| ||||||
Db       1431 TTTACGAACCCTCAGAATATTTCTGATAGAGGTACCGCTAACTATAGTCAACCTTATGAG 1490

Qy       1321 TCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACCAGAAACAACAGAACGA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1491 TCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACCAGAAACAACAGAACGA 1550

Qy       1381 CCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCTCATTTCACAATCTAGG 1440
              ||||||||||||| || ||||| |||||||||| |||||  | |||| |||||| |||
Db       1551 CCAAATTATGAATCTTACAGTCACAGGTTATCTCATATAGGTATAATTTTACAATCCAGG 1610

Qy       1441 GTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGATCGTACAAATACCATTAGT 1500
              ||| ||||||| |||||||||||||||| |||||||||||||||| ||||| ||| |
Db       1611 GTGAATGTACCGGTATATTCTTGGACGCATCGTAGTGCAGATCGTACGAATACGATTGGA 1670

Qy       1501 TCAGATAGCATAACACAAATACCATTGGTAAAATCATTCAACCTTAATTCAGGTACCTCT 1560
              || |||| || || ||||| ||| |||||||| ||| | | ||| | ||||||| ||
Db       1671 CCAAATAGAATCACCCAAATCCCAATGGTAAAAGCATCCGAACTTCCTCAAGGTACCACT 1730

Qy       1561 GTAGTCAGTGGCCCAGGATTTACAGGAGGGGATATAATCCGAACTAACGTTAATGGTAGT 1620
              || || || || |||||||||| || |||||||| | |||| | || |||| |
Db       1731 GTTGTTAGAGGACCAGGATTTACTGGTGGGGATATTCTTCGAAGAACGAATACTGGTGGA 1790

Qy       1621 GTACTAAGTATGGGTCTTAATTTTAATAATACATCATTACAGCGGTATCGCGTGAGAGTT 1680
              | |  || | | | | |||| ||| | ||| | ||||| | || |
Db       1791 TTTGGACCGATAAGAGTAACTGTTAACGGACCATTAACACAAAGATATCGTATAGGATTC 1850

Qy       1681 CGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGTCGGAGGGAGTACTACTTTT 1740
              || |||||| | || |  | |  |  ||| |  |||| | ||||  |
Db       1851 CGCTATGCTTCAACTGTAGATTTTGATTTCTTTGTATCACGTGGAGGTACTACTGTAAAT 1910

Qy       1741 GATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAATCATTTAGA 1800
              ||   ||||||  |||| ||||      ||    | | ||   |  |||
Db       1911 AATTTTAGATTCCTACGTACAATGAACAGTGGAGACGAACTAAAATACGGAAATTTTGTG 1970

Qy       1801 TTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAA---ACTGCTGGAATAAGT 1857
                  | ||| ||  |  | ||| |   |  | ||||   |   | |||   |
Db       1971 AGACGTGCTTTTACTACACCTTTTACTTTTACACAAATTCAAGATATAATTCGAACGTCT 2030

Qy       1858 ATAAGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATTGAATTCATTCCAATT 1917
              ||      |  || |      |  | | ||||||||||||| | |||||| ||
Db       2031 ATTCAAGGCCTTAGTGGAAATGGGGAAGTGTATATAGATAAAATTGAAATTATTCCAGTT 2090

Qy       1918 ACTGCAACCTTCGAAGCAGAATACGATTTAGAAAGGGCGCAAGAGGCGGTGAATGCTCTG 1977
              |||||||||||||||||||||| |||||||||| ||||||||||||||||||||||||
Db       2091 ACTGCAACCTTCGAAGCAGAATATGATTTAGAAAGAGCGCAAGAGGCGGTGAATGCTCTG 2150
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Qy       1978 TTTACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATTGATCAA 2037
Db       2151 TTTACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATTGATCAA 2210

Qy       2038 GTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAAGAGAGAATTA 2097
Db       2211 GTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTGGATGAAAAGAGAGAATTA 2270

Qy       2098 CTTGAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAACTTACTCCAAGATCCA 2157
Db       2271 CTTGAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAACTTACTCCAAGATCCA 2330

Qy       2158 AACTTCACATCCATCAATAAGCAACCAGACTTCATATCTACTAATGAGCAATCGAATTTC 2217
Db       2331 AACTTCACATCCATCAATAAGCAACCAGACTTCATATCTACTAATGAGCAATCGAATTTC 2390

Qy       2218 ACATCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTACAATCCAG 2277
Db       2391 ACATCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTACCATCCAG 2450

Qy       2278 GAAGGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGACTTTTAATGAGTGT 2337
Db       2451 GAAGGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGTACTTTTAATGAGTGT 2510

Qy       2338 TATCCGACGTATTTATATCAAAAAATAGGAGAGTCGGAATTAAAAGCTTATACTCGCTAC 2397
Db       2511 TATCCGACGTATTTATATCAAAAAATAGGGGAGTCGGAATTAAAAGCTTATACTCGCTAC 2570

Qy       2398 CAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAAT 2457
Db       2571 CAATTAAGAGGTTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAAT 2630

Qy       2458 GCGAAACATGAAACATTGGATGTTCCAGGTACCGAGTCCGTATGGCCGCTTTCAGTTGAA 2517
Db       2631 GCGAAACATGAAACATTGGATGTTCCAGGTACCGAGTCCCTATGGCCGCTTTCAGTTGAA 2690

Qy       2518 AGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTTTGAATGGAATCCT 2577
Db       2691 AGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTTTGAATGGAATCCT 2750

Qy       2578 GATCTAGATTGTTCCTGCAGAGATGGAGAAAAATGTGCGCATCATTCCCATCATTTCTCT 2637
Db       2751 GATCTAGATTGTTCCTGCAGAGATGGAGAAAAATGTGCGCATCATTCCCATCATTTCTCT 2810

Qy       2638 TTGGATATTGATATTGGATGCACAGACTTGCATGAGAATCTAGGCGTGTGGGTGGTATTC 2697
Db       2811 TTGGATATTGATGTTGGATGCACAGACTTGCATGAGAATCTAGGCGTGTGGGTGGTATTC 2870

Qy       2698 AAGATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAATCTGGAATTTATTGAAGAGAAA 2757
Db       2871 AAGATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAATCTGGAATTTATTGAAGAGAAA 2930

Qy       2758 CCATTATTAGGAGAAGCACTGTCTCGTGTGAAGAGAGCAGAGAAAAAATGGAGAGACAAA 2817
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Db       2991 CGTGAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAGAAGCTGTGGAT 3050

Qy       2878 GCTTTATTTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTGGCATGATT 2937
Db       3051 GCTTTATTCGTAGATTCTCAATATGATAGATTACAAGCGGATACAAACATCGGCATGATT 3110

Qy       2938 CATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCTTATCTGTCAGAATTATCTGTT 2997
Db       3111 CATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCGTATCTTTCAGAATTACCTGTT 3170

Qy       2998 ATCCCGGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCGCATTATCACTGCAATC 3057
Db       3171 ATCCCAGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCACATTATCACTGCAATC 3230

Qy       3058 TCCCTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTAGCATGC 3117
Db       3231 TCCTTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTAACATGT 3290

Qy       3118 TGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCCTTGTTATC 3177
Db       3291 TGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCATCGTTCTGACCTTGTTATC 3350

Qy       3178 CCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGCTATATC 3237
Db       3351 CCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGTGTGGCTATATC 3410

Qy       3238 CTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGTTGTGTAACGATCCATGAAATC 3297
Db       3411 CTTCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGCTGCGTAACGATCCATGAAATC 3470

Qy       3298 GAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTATCCAACG 3357
Db       3471 GAGAACAATACAGACGAACTAAAATTTAAAAACCGTGAAGAAGAGGAAGTGTATCCAACG 3530

Qy       3358 GATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGC----------AGTA 3405
Db       3531 GATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCTGGATGCGCAGATGCA 3590

Qy       3406 TGTAATTCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTT 3465
Db       3591 TGTAATTCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTT 3650

Qy       3466 AATTACAAACCGACTTATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGT 3525
Db       3651 AATTACAAACCGACTTATGAAGAAGAAACGTATACAGATGTAAGAAGAGATAATCATTGT 3710

Qy       3526 GAATATGACAGAGGGTATGTGAATTATCCACCACTACCAGCTGGTTATATGACAAAAGAA 3585
Db       3711 GAATATGACAGAGGGTATGTCAATTATCCACCAGTACCAGCTGGTTATGTGACAAAAGAA 3770

Qy       3586 TTAGAATACTTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGGGAAG 3645
Db       3771 TTAGAATACTTCCCAGAAACAGATACAGTATGGATTGAGATTGGAGAAACGGAAGGAAAG 3830

Qy       3646 TTTATTGTAGACAGCGTGGAATTACTCCTTATGGAGGAATAG 3687
Db       3831 TTTATTGTAGATAGCGTGGAATTACTCCTCATGGAAGAATAG 3872
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RESULT 6
US-08-100-709-3
; Sequence 3, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729

```
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Egolf, Christopher
;      REGISTRATION NUMBER:  27633
;      REFERENCE/DOCKET NUMBER:  7205-49
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-757-1590
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3934 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  67..3756
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  2253..2272
US-08-100-709-3

  Query Match             72.9%;  Score 2687.2;  DB 1;  Length 3934;
  Best Local Similarity   83.5%;  Pred. No. 0;
  Matches 3088;  Conservative    0;  Mismatches  593;  Indels   15;  Gaps    3;

Qy          1 TTGACTTCAAATAGGAAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAGCTGTA 60
Db         67 TTGACTTCAAATAGGAAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAACGGTA 126

Qy         61 TCGAATCATTCCACACAAATGGATCTATCACCAGATGCTCGTATTGAGGATTCTTTGTGT 120
Db        127 TCGAATCCTTCCACGCAAATGAATCTATCACCAGATGCTCGTATTGAAGATAGCTTGTGT 186

Qy        121 ATAGCCGAGGGGAATAATATCAATCCACTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
Db        187 GTAGCCGAGGTGAACAATATTGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATA 246

Qy        181 AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGT 240
Db        247 AACATAGCTGGTAGAATATTGGGCGTATTAGGTGTGCCGTTTGCTGGACAACTAGCTAGT 306

Qy        241 TTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTC 300
Db        307 TTTTATAGTTTTCTTGTTGGGGAATTATGGCCTAGTGGCAGAGATCCATGGGAAATTTTC 366

Qy        301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCA 360
Db        367 CTGGAACATGTAGAACAACTTATAAGACAACAAGTAACAGAAAATACTAGGAATACGGCT 426

Qy        361 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
Db        427 ATTGCTCGATTAGAAGGTCTAGGAAGAGGCTATAGATCTTACCAGCAGGCTCTTGAAACT 486

Qy        421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGCC 480
Db        487 TGGTTAGATAACCGAAATGATGCAAGATCAAGAAGCATTATTCTTGAGCGCTATGTTGCT 546

Qy        481 TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA 540
Db        547 TTAGAACTTGACATTACTACTGCTATACCGCTTTTCAGAATACGAAATGAAGAAGTTCCA 606

Qy        541 TTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATTGAGAGATGCCTCT 600
Db        607 TTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATTGAGAGACGCATCC 666

Qy        601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTATTATGAGCGCCAA 660
Db        667 CTTTTTGGTAGTGAATGGGGGATGGCATCTTCCGATGTTAACCAATATTACCAAGAACAA 726

Qy        661 GTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT 720
Db        727 ATCAGATATACAGAGGAATATTCTAACCATTGCGTACAATGGTATAATACAGGGCTAAAT 786

Qy        721 AGCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCAATTCCGTAGAGATCTA 780
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Qy        781 ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840
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Qy        841 ATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGCAATTGGAGCAACAGGG 900
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Qy        901 GTAAAT------ATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTTTCCGCT 954
Db        967 GCACCTTCAGGATTTGCAAGTACGAATTGGTTTAATAATAATGCACCATCGTTTTCTGCC 1026

Qy        955 ATAGAGACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACAACTTACAATT 1014
Db       1027 ATAGAGGCTGCCATTTTCAGGCCTCCGCATCTACTTGATTTTCCAGAACAACTTACAATT 1086

Qy       1015 TTTAGCACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGGCGGGGGCACACA 1074
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Qy       1075 ATTCAATCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGTCTACCA---AT 1131
Db       1147 CTTAACTTCCGCCCAATAGGAGGGACATTAAATACCTCAACACAAGGACTTACTAATAAT 1206

Qy       1132 ACTTCTATTAATCCTGTAAGATTATCATTCTTCTCTCGAGACGTATATTGGACTGAATCA 1191
Db       1207 ACTTCAATTAATCCTGTAACATTACAGTTTACGTCTCGAGACGTTTATAGAACAGAATCA 1266

Qy       1192 TATGCAGGAGTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCCTACTGTT 1251
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Qy       1312 CCCTATGAGTCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACCAGAAACA 1371
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Qy       1372 ACAGAACGACCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCTCATTTCA 1431
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Qy       1432 CAATCTAGGGTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGATCGTACAAAT 1491
Db       1501 GGAAACACTTTGAGAGCACCAGTCTATTCTTGGACGCATCGTAGTGCAGATCGTACGAAT 1560

Qy       1492 ACCATTAGTTCAGATAGCATAACACAAATACCATTGGTAAAATCATTCAACCTTAATTCA 1551
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Qy       1552 GGTACCTCTGTAGTCAGTGGCCCAGGATTTACAGGAGGGGATATAATCCGAACTAACGTT 1611
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Qy       1612 AATGGTAGTGTACTAAGTATGGGTCTTAATTTTAATAATACATCATTACAGCGGTATCGC 1671
Db       1681 ACGGGTACATTTGGAGATATACGATTAAATATTAATGTGCCATTATCCCAAAGATATCGC 1740

Qy       1672 GTGAGAGTTCGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGTCGGAGGGAGT 1731
Db       1741 GTAAGGATTCGTTATGCTTCTACTACAGATTTACAATTTTCACGAGAATTAATGGAACC 1800

Qy       1732 ACTACTTTTGATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAA 1791
Db       1801 ACTGTTAATATTGGTAATTTCTCAAGAACTATGAATAGGGGGATAATTTAGAATATAGA 1860
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Qy       1792 TCATTTAGATTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGA 1851
Db       1861 AGTTTTAGAACTGCAGGATTTAGTACTCCTTTTAATTTTTTAAATGCCCAAAGCACATTC 1920

Qy       1852 ATAAGTATAAGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATTGAATTCATT 1911
Db       1921 ACATTGGGTGCTCAGAGTTTTTCAAATCAGGAAGTTTATATAGATAGAGTCGAATTTGTT 1980

Qy       1912 CCAATTACTGCAACCTTCGAAGCAGAATACGATTTAGAAAGGGCGCAAGAGGCGGTGAAT 1971
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Qy       1972 GCTCTGTTTACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATT 2031
Db       2041 GCTCTGTTTACTTCTACAAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATT 2100

Qy       2032 GATCAAGTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAAGAGA 2091
Db       2101 GACCAAGTGTCCAATATGGTGGCATGTTTATCAGATGAATTTTGCTTGGATGAGAAGCGA 2160

Qy       2092 GAATTACTTGAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAACTTACTCCAA 2151
Db       2161 GAATTATTTGAGAAAGTGAAATATGCGAAGCGACTCAGTGATGAAAGAAACTTACTCCAA 2220

Qy       2152 GATCCAAACTTCACATCCATCAATAAGCAACCAGACTTCATATCTACTAATGAGCAATCG 2211
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Qy       2212 AATTTCACATCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTACA 2271
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Qy       2392 CGCTACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGT 2451
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Qy       2452 TATAATGCGAAACATGAAACATTGGATGTTCCAGGTACCGAGTCCGTATGGCCGCTTTCA 2511
Db       2521 TACAATGCAAAGCATGAAACATTGGATGTTCCAGGTACCGATTCCCTATGGCCGCTTTCA 2580

Qy       2512 GTTGAAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTTTGAATGG 2571
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Qy       2572 AATCCTGATCTAGATTGTTCCTGCAGAGATGGAGAAAAATGTGCGCATCATTCCCATCAT 2631
Db       2641 AATCCTGATCTAGATTGTTCCTGCAGAGATGGAGAAAGATGTGCGCATCATTCCCATCAT 2700

Qy       2632 TTCTCTTTGGATATTGATATTGGATGCACAGACTTGCATGAGAATCTAGGCGTGTGGGTG 2691
Db       2701 TTCACTTTGGATATTGATGTTGGGTGCACAGACTTGCATGAGAACCTAGGCGTGTGGGTG 2760

Qy       2692 GTATTCAAGATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAATCTGGAATTTATTGAA 2751
Db       2761 GTATTCAAGATTAAGACGCAGGAAGGTTATGCAAGATTAGGAAATCTGGAATTTATCGAA 2820

Qy       2752 GAGAAACCATTATTAGGAGAAGCACTGTCTCGTGTGAAGAGAGCAGAGAAAAAATGGAGA 2811
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Qy       2872 GTGGATGCTTTATTTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTGGC 2931
Db       2941 GTGGATGCTTTATTCGTAGATTCTCAATATGATCAATTACAAGCGGATACAAACATTGGC 3000

Qy       2932 ATGATTCATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCTTATCTGTCAGAATTA 2991
Db       3001 ATGATTCATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCGTATCTTTCAGAATTA 3060

Qy       2992 TCTGTTATCCCGGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCGCATTATCACT 3051
Db       3061 CCTGTTATCCCAGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCACATTATCACT 3120

Qy       3052 GCAATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTA 3111
Db       3121 GCAATGTCCTTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTA 3180

Qy       3112 GCATGCTGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCCTT 3171
Db       3181 ACATGTTGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCATCGTTCTGACCTT 3240

Qy       3172 GTTATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGC 3231
Db       3241 GTTATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGC 3300

Qy       3232 TATATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGTTGTGTAACGATCCAT 3291
Db       3301 TATATCCTTCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGCTGCGTAACGATCCAT 3360

Qy       3292 GAAATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTAT 3351
Db       3361 GAAATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTAT 3420

Qy       3352 CCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGTATGTAAT 3411
Db       3421 CCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGCATGTAAT 3480

Qy       3412 TCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTAC 3471
Db       3481 TCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTAC 3540

Qy       3472 AAACCGACTTATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGTGAATAT 3531
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Qy       3532 GACAGAGGGTATGTGAATTATCCACCACTACCAGCTGGTTATATGACAAAAGAATTAGAA 3591
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Qy       3592 TACTTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGGGAAGTTTATT 3651
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Qy       3652 GTAGACAGCGTGGAATTACTCCTTATGGAGGAATAG 3687
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RESULT 7
US-08-176-865-3
; Sequence 3, Application US/08176865
; Patent No. 5616319
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia

; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,865
; FILING DATE: 30-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3934 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 67..3756
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2253..2272
US-08-176-865-3

Query Match 72.9%; Score 2687.2; DB 1; Length 3934;
Best Local Similarity 83.5%; Pred. No. 0;
Matches 3088; Conservative 0; Mismatches 593; Indels 15; Gaps 3;

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Qy        181 AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGT 240
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Db        307 TTTTATAGTTTTCTTGTTGGGGAATTATGGCCTAGTGGCAGAGATCCATGGGAAATTTTC 366

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Qy        361 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
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Db        487 TGGTTAGATAACCGAAATGATGCAAGATCAAGAAGCATTATTCTTGAGCGCTATGTTGCT 546

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Db        727 ATCAGATATACAGAGGAATATTCTAACCATTGCGTACAATGGTATAATACAGGGCTAAAT 786

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Db        787 AACTTAAGAGGGACAAATGCTGAAAGTTGGTTGCGGTATAATCAATTCCGTAGAGACCTA 846

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Qy        955 ATAGAGACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACAACTTACAATT 1014
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Db       1027 ATAGAGGCTGCCATTTTCAGGCCTCCGCATCTACTTGATTTTCCAGAACAACTTACAATT 1086

Qy       1015 TTTAGCACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGGCGGGGGCACACA 1074
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Db       1087 TACAGTGCATCAAGCCGTTGGAGTAGCACTCAACATATGAATTATTGGGTGGGACATAGG 1146

Qy       1075 ATTCAATCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGTCTACCA---AT 1131
              || | |  || ||||||||||    |||||||||||||||| || ||   ||| |   ||
Db       1147 CTTAACTTCCGCCCAATAGGAGGGACATTAAATACCTCAACACAAGGACTTACTAATAAT 1206

Qy       1132 ACTTCTATTAATCCTGTAAGATTATCATTCTTCTCTCGAGACGTATATTGGACTGAATCA 1191
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Db       1207 ACTTCAATTAATCCTGTAACATTACAGTTTACGTCTCGAGACGTTTATAGAACAGAATCA 1266

Qy       1192 TATGCAGGAGTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCCTACTGTT 1251
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Db       1267 AATGCAGGGACAAATAT------ACTATTTACTACTCCTGTGAATGGAGTACCTTGGGCT 1320

Qy       1252 AGATTTAATTTTAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGTCAA 1311
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Db       1321 AGATTTAATTTTATAAACCCTCAGAATATTTATGAAAGAGGCGCCACTACCTACAGTCAA 1380

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Db       1381 CCGTATCAGGGAGTTGGGATTCAATTATTTGATTCAGAAACTGAATTACCACCAGAAACA 1440

Qy       1372 ACAGAACGACCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCTCATTTCA 1431
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Db       1441 ACAGAACGACCAAATTATGAATCATATAGTCATAGATTATCTCATATAGGACTAATCATA 1500

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Db       1561 ACGATTGGACCAAATAGAATTACACAAATACCATTGGTAAAAGCACTGAATCTTCATTCA 1620

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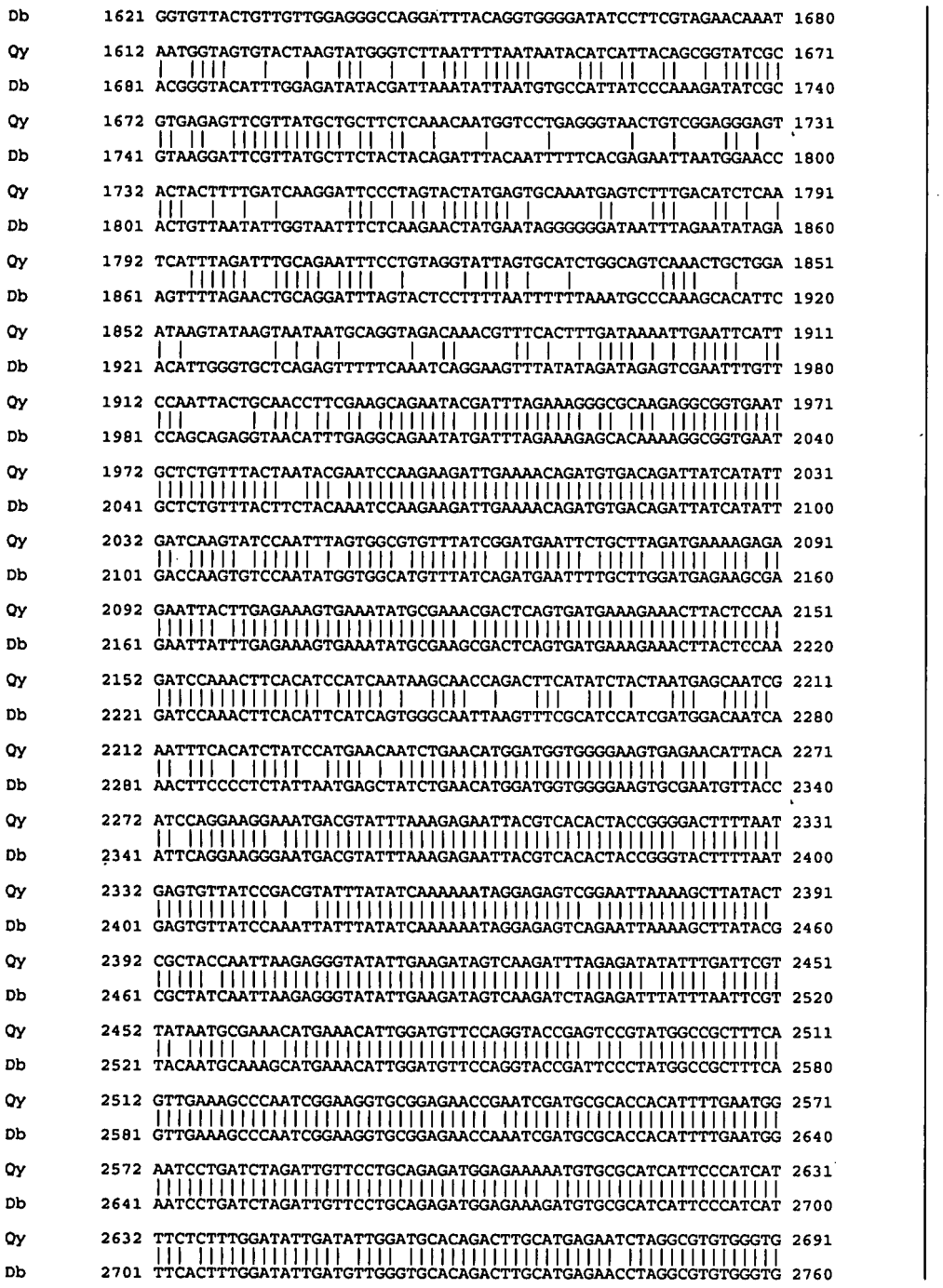

RESULT 8
US-08-474-038-3
; Sequence 3, Application US/08474038

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; Patent No. 5679343
;  GENERAL INFORMATION:
;    APPLICANT:  Donovan, William P.
;    APPLICANT:  Tan, Yuping
;    APPLICANT:  Jany, Christine S.
;    APPLICANT:  Gonzalez Jr., Jose M.
;    TITLE OF INVENTION:  BACILLUS THURINGIENSIS cryET4 AND cryET5
;    TITLE OF INVENTION:  TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Panitch Schwarze Jacobs & Nadel c/o A.S.
;      ADDRESSEE:  Nadel
;      STREET:  1601 Market Street, 36th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,038
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/176,865
;      FILING DATE:  30-DEC-1993
;      APPLICATION NUMBER:  US 08/100,709
;      FILING DATE:  29-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Egolf, Christopher
;      REGISTRATION NUMBER:  27633
;      REFERENCE/DOCKET NUMBER:  7205-49
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-757-1590
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3934 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  67..3756
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  2253..2272
US-08-474-038-3

  Query Match             72.9%;  Score 2687.2;  DB 1;  Length 3934;
  Best Local Similarity   83.5%;  Pred. No. 0;
  Matches 3088;  Conservative    0;  Mismatches  593;  Indels   15;  Gaps    3;

Qy          1 TTGACTTCAAATAGGAAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAGCTGTA 60
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Db         67 TTGACTTCAAATAGGAAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAACGGTA 126

Qy         61 TCGAATCATTCCACACAAATGGATCTATCACCAGATGCTCGTATTGAGGATTCTTTGTGT 120
              ||||||| |||||| |||||| |||||||||||||||||||||||| |||    ||||||
Db        127 TCGAATCCTTCCACGCAAATGAATCTATCACCAGATGCTCGTATTGAAGATAGCTTGTGT 186

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              |||||||||| ||| |||||  ||||| ||||||||||||||||||||||||||||||
Db        187 GTAGCCGAGGTGAACAATATTGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATA 246

Qy        181 AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGT 240
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Db        247 AACATAGCTGGTAGAATATTGGGCGTATTAGGTGTGCCGTTTGCTGGACAACTAGCTAGT 306

Qy        241 TTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTC 300
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Qy        301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCA 360
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Qy        361 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
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Qy        421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGCC 480
              ||| |||| |||||  |||||||||||| | |||||  || ||  |   |  ||| | ||
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Qy        481 TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA 540
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Db        547 TTAGAACTTGACATTACTACTGCTATACCGCTTTTCAGAATACGAAATGAAGAAGTTCCA 606

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Db        667 CTTTTTGGTAGTGAATGGGGGATGGCATCTTCCGATGTTAACCAATATTACCAAGAACAA 726

Qy        661 GTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT 720
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Qy        721 AGCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCAATTCCGTAGAGATCTA 780
              | ||| |||||||||||||| | ||||||| |||| ||||||||||||||||||| |||
Db        787 AACTTAAGAGGGACAAATGCTGAAAGTTGGTTGCGGTATAATCAATTCCGTAGAGACCTA 846

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Qy       1075 ATTCAATCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGTCTACCA---AT 1131
              || | |  || ||||||||||   |||||||||||||| || ||   ||| |   ||
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Qy       1132 ACTTCTATTAATCCTGTAAGATTATCATTCTTCTCTCGAGACGTATATTGGACTGAATCA 1191
              ||||| |||||||||||| ||||   ||     |||||||||| ||| | || ||||||
Db       1207 ACTTCAATTAATCCTGTAACATTACAGTTTACGTCTCGAGACGTTTATAGAACAGAATCA 1266

Qy       1192 TATGCAGGAGTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCCTACTGTT 1251
              |||||||       | |      | | |      |  ||| |  |||| || |||   | |
Db       1267 AATGCAGGGACAAATAT------ACTATTTACTACTCCTGTGAATGGAGTACCTTGGGCT 1320

Qy       1252 AGATTTAATTTTAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGTCAA 1311
              ||||||||||||  |||||||||||| || |||||||||  |  ||| ||| ||||||
Db       1321 AGATTTAATTTTATAAACCCTCAGAATATTTATGAAAGAGGCGCCACTACCTACAGTCAA 1380

Qy       1312 CCCTATGAGTCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACCAGAAACA 1371
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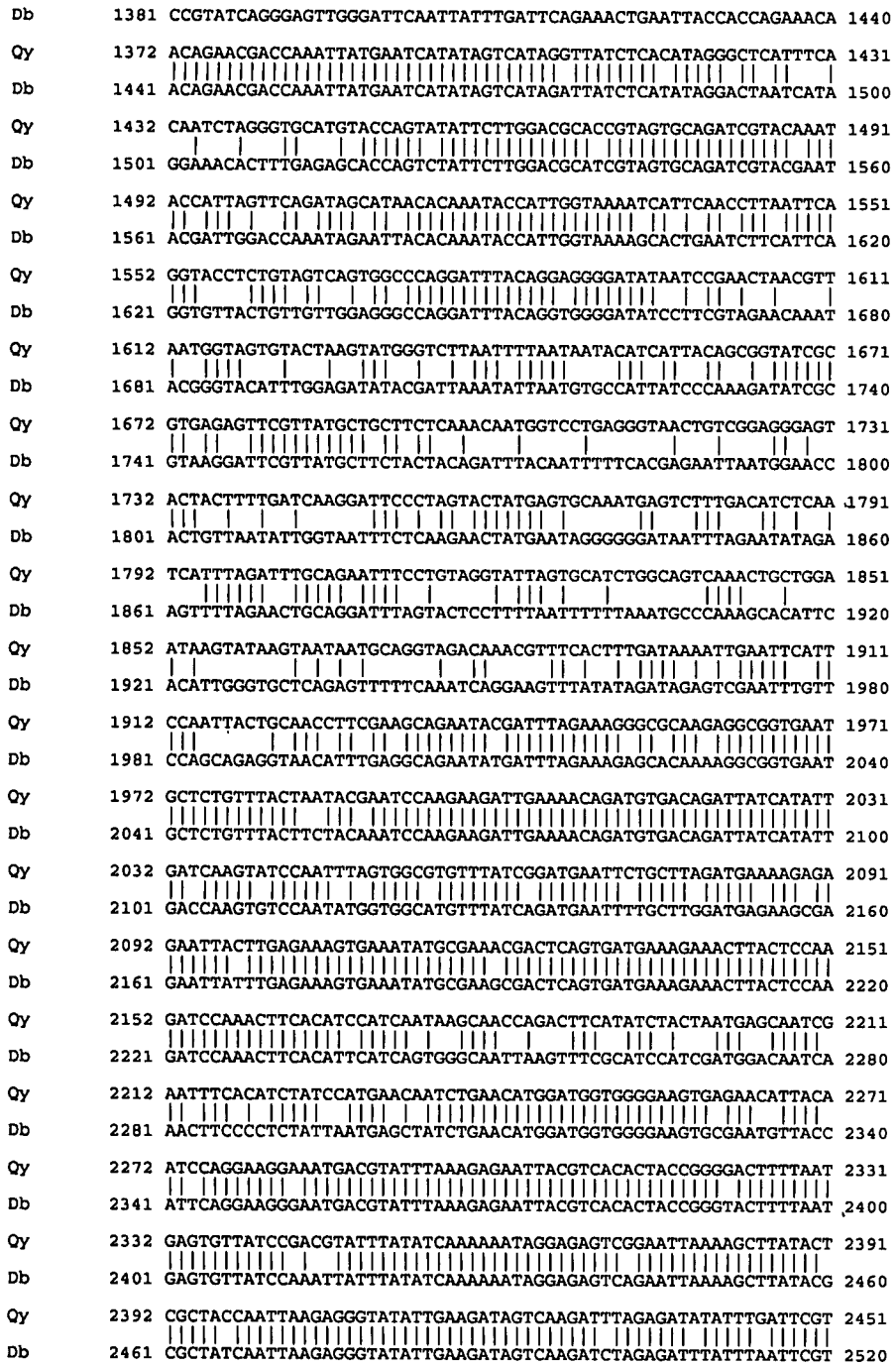
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Qy 1372 ACAGAACGACCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCTCATTTCA 1431
Db 1441 ACAGAACGACCAAATTATGAATCATATAGTCATAGATTATCTCATATAGGACTAATCATA 1500
Qy 1432 CAATCTAGGGTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGATCGTACAAAT 1491
Db 1501 GGAAACACTTTGAGAGCACCAGTCTATTCTTGGACGCATCGTAGTGCAGATCGTACGAAT 1560
Qy 1492 ACCATTAGTTCAGATAGCATAACACAAATACCATTGGTAAAATCATTCAACCTTAATTCA 1551
Db 1561 ACGATTGGACCAAATAGAATTACACAAATACCATTGGTAAAAGCACTGAATCTTCATTCA 1620
Qy 1552 GGTACCTCTGTAGTCAGTGGCCCAGGATTTACAGGAGGGGATATAATCCGAACTAACGTT 1611
Db 1621 GGTGTTACTGTTGTTGGAGGGCCAGGATTTACAGGTGGGGATATCCTTCGTAGAACAAAT 1680
Qy 1612 AATGGTAGTGTACTAAGTATGGGTCTTAATTTTAATAATACATCATTACAGCGGTATCGC 1671
Db 1681 ACGGGTACATTTGGAGATATACGATTAAATATTAATGTGCCATTATCCCAAAGATATCGC 1740
Qy 1672 GTGAGAGTTCGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGTCGGAGGGAGT 1731
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Qy 1732 ACTACTTTTGATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAA 1791
Db 1801 ACTGTTAATATTGGTAATTTCTCAAGAACTATGAATAGGGGGGATAATTTAGAATATAGA 1860
Qy 1792 TCATTTAGATTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGA 1851
Db 1861 AGTTTTAGAACTGCAGGATTTAGTACTCCTTTTAATTTTTTAAATGCCCAAAGCACATTC 1920
Qy 1852 ATAAGTATAAGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATTGAATTCATT 1911
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Db 1981 CCAGCAGAGGTAACATTTGAGGCAGAATATGATTTAGAAAGAGCACAAAAGGCGGTGAAT 2040
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Qy 2032 GATCAAGTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAAGAGA 2091
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Qy 2092 GAATTACTTGAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAACTTACTCCAA 2151
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Qy 2272 ATCCAGGAAGGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGACTTTTAAT 2331
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Qy 2332 GAGTGTTATCCGACGTATTTATATCAAAAAATAGGAGAGTCGGAATTAAAAGCTTATACT 2391
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Qy 2392 CGCTACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGT 2451
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Db 2521 TACAATGCAAAGCATGAAACATTGGATGTTCCAGGTACCGATTCCCTATGGCCGCTTTCA 2580
Qy 2512 GTTGAAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTTTGAATGG 2571
Db 2581 GTTGAAAGCCCAATCGGAAGGTGCGGAGAACCAAATCGATGCGCACCACATTTTGAATGG 2640
Qy 2572 AATCCTGATCTAGATTGTTCCTGCAGAGATGGAGAAAAATGTGCGCATCATTCCCATCAT 2631
Db 2641 AATCCTGATCTAGATTGTTCCTGCAGAGATGGAGAAAGATGTGCGCATCATTCCCATCAT 2700
Qy 2632 TTCTCTTTGGATATTGATATTGGATGCACAGACTTGCATGAGAATCTAGGCGTGTGGGTG 2691
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Db 2761 GTATTCAAGATTAAGACGCAGGAAGGTTATGCAAGATTAGGAAATCTGGAATTTATCGAA 2820
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Qy 2992 TCTGTTATCCCGGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCGCATTATCACT 3051
Db 3061 CCTGTTATCCCAGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCACATTATCACT 3120
Qy 3052 GCAATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTA 3111
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Qy 3172 GTTATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGC 3231
Db 3241 GTTATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGC 3300
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Db 3301 TATATCCTTCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGCTGCGTAACGATCCAT 3360
Qy 3292 GAAATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTAT 3351
Db 3361 GAAATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTAT 3420
Qy 3352 CCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGTATGTAAT 3411
Db 3421 CCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGCATGTAAT 3480
Qy 3412 TCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTAC 3471
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Db       3601 GACAGAGGGTATGTGAATTATCCACCAGTACCAGCTGGTTATGTGACAAAAGAATTAGAA 3660

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Db       3661 TACTTCCCAGAAACAGATACAGTATGGATTGAGATTGGAGAAACGGAAGGAAAGTTTATT 3720

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RESULT 9
US-08-779-046-3
; Sequence 3, Application US/08779046
; Patent No. 5854053
;  GENERAL INFORMATION:
;    APPLICANT:  Donovan, William P.
;    APPLICANT:  Tan, Yuping
;    APPLICANT:  Jany, Christine S.
;    APPLICANT:  Gonzalez Jr., Jose M.
;    TITLE OF INVENTION:  BACILLUS THURINGIENSIS cryET4 AND cryET5
;    TITLE OF INVENTION:  TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Panitch Schwarze Jacobs & Nadel c/o A.S.
;      ADDRESSEE:  Nadel
;      STREET:  1601 Market Street, 36th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/779,046
;      FILING DATE:  06-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/100,709
;      FILING DATE:  29-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Egolf, Christopher
;      REGISTRATION NUMBER:  27633
;      REFERENCE/DOCKET NUMBER:  7205-49
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-757-1590
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3934 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  67..3756
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  2253..2272
US-08-779-046-3

  Query Match             72.9%;  Score 2687.2;  DB 2;  Length 3934;
  Best Local Similarity   83.5%;  Pred. No. 0;
  Matches 3088;  Conservative    0;  Mismatches  593;  Indels   15;  Gaps    3;

Qy          1 TTGACTTCAAATAGGAAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAGCTGTA 60
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Qy        721 AGCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCAATTCCGTAGAGATCTA 780
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Qy        781 ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840
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Qy        901 GTAAAT------ATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTTTCCGCT 954
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Qy        955 ATAGAGACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACAACTTACAATT 1014
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Db       1027 ATAGAGGCTGCCATTTTCAGGCCTCCGCATCTACTTGATTTTCCAGAACAACTTACAATT 1086

Qy       1015 TTTAGCACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGGCGGGGGCACACA 1074
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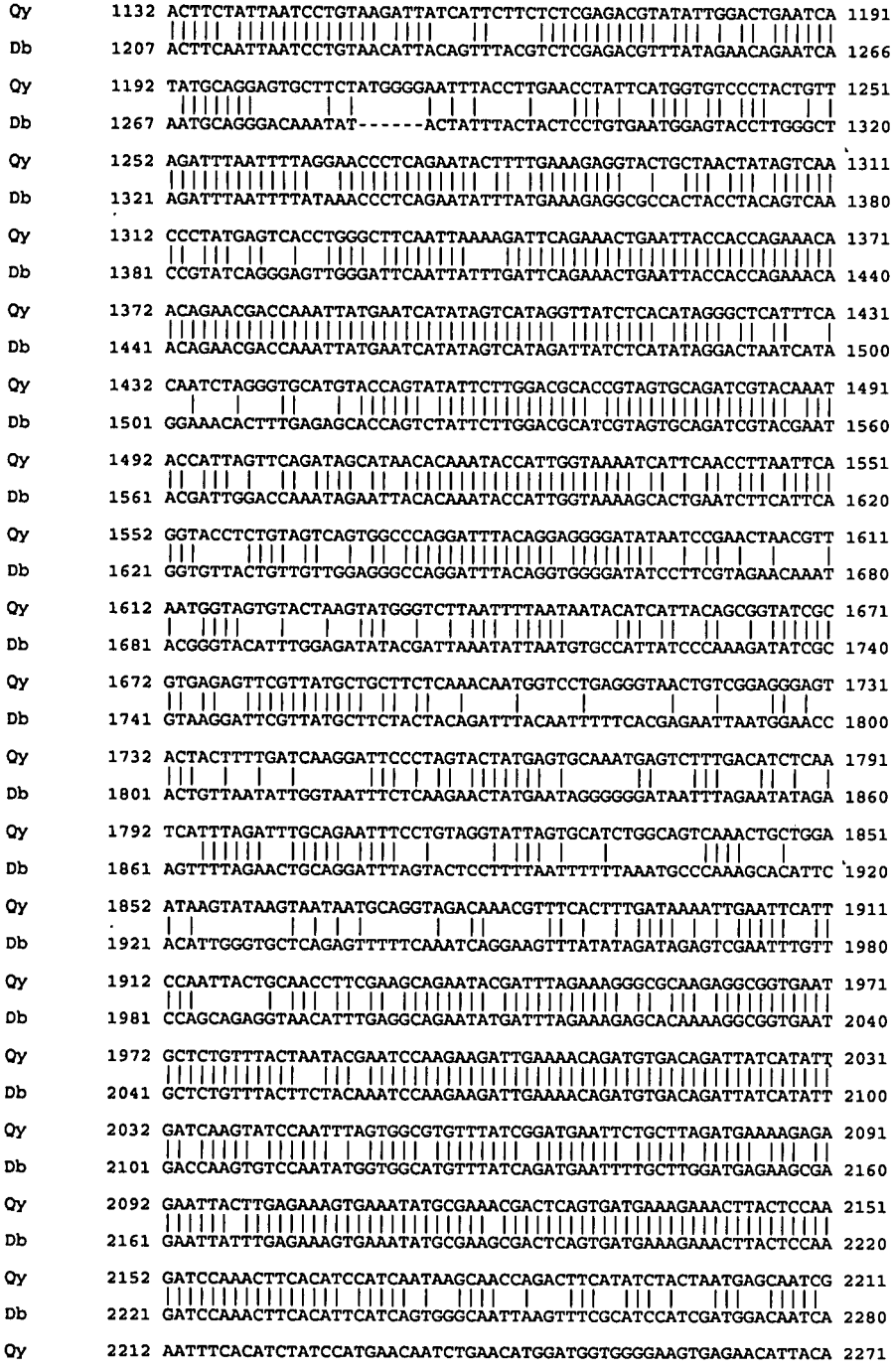
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Qy 1252 AGATTTAATTTTAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGTCAA 1311
Db 1321 AGATTTAATTTTATAAACCCTCAGAATATTTATGAAAGAGGCGCCACTACCTACAGTCAA 1380
Qy 1312 CCCTATGAGTCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACCAGAAACA 1371
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Qy 1372 ACAGAACGACCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCTCATTTCA 1431
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Db 2161 GAATTATTTGAGAAAGTGAAATATGCGAAGCGACTCAGTGATGAAAGAAACTTACTCCAA 2220
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Qy 3052 GCAATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTA 3111
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Db       3481 TCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTAC 3540

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RESULT 10
US-08-881-340-3
; Sequence 3, Application US/08881340
; Patent No. 5942658
;  GENERAL INFORMATION:
;    APPLICANT:  Donovan, William P.
;    APPLICANT:  Tan, Yuping
;    APPLICANT:  Jany, Christine S.
;    APPLICANT:  Gonzalez Jr., Jose M.
;    TITLE OF INVENTION:  BACILLUS THURINGIENSIS cryET4 AND cryET5
;    TITLE OF INVENTION:  TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Panitch Schwarze Jacobs & Nadel c/o A.S.
;      ADDRESSEE:  Nadel
;      STREET:  1601 Market Street, 36th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/881,340
;      FILING DATE:  24-JUN-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/100,709
;      FILING DATE:  29-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Egolf, Christopher
;      REGISTRATION NUMBER:  27633
;      REFERENCE/DOCKET NUMBER:  7205-49
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-757-1590
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3934 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
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;      NAME/KEY:  misc_feature
;      LOCATION:  2253..2272
US-08-881-340-3

  Query Match             72.9%;  Score 2687.2;  DB 2;  Length 3934;
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  Matches 3088;  Conservative    0;  Mismatches  593;  Indels   15;  Gaps    3;

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Qy        901 GTAAAT------ATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTTTCCGCT 954
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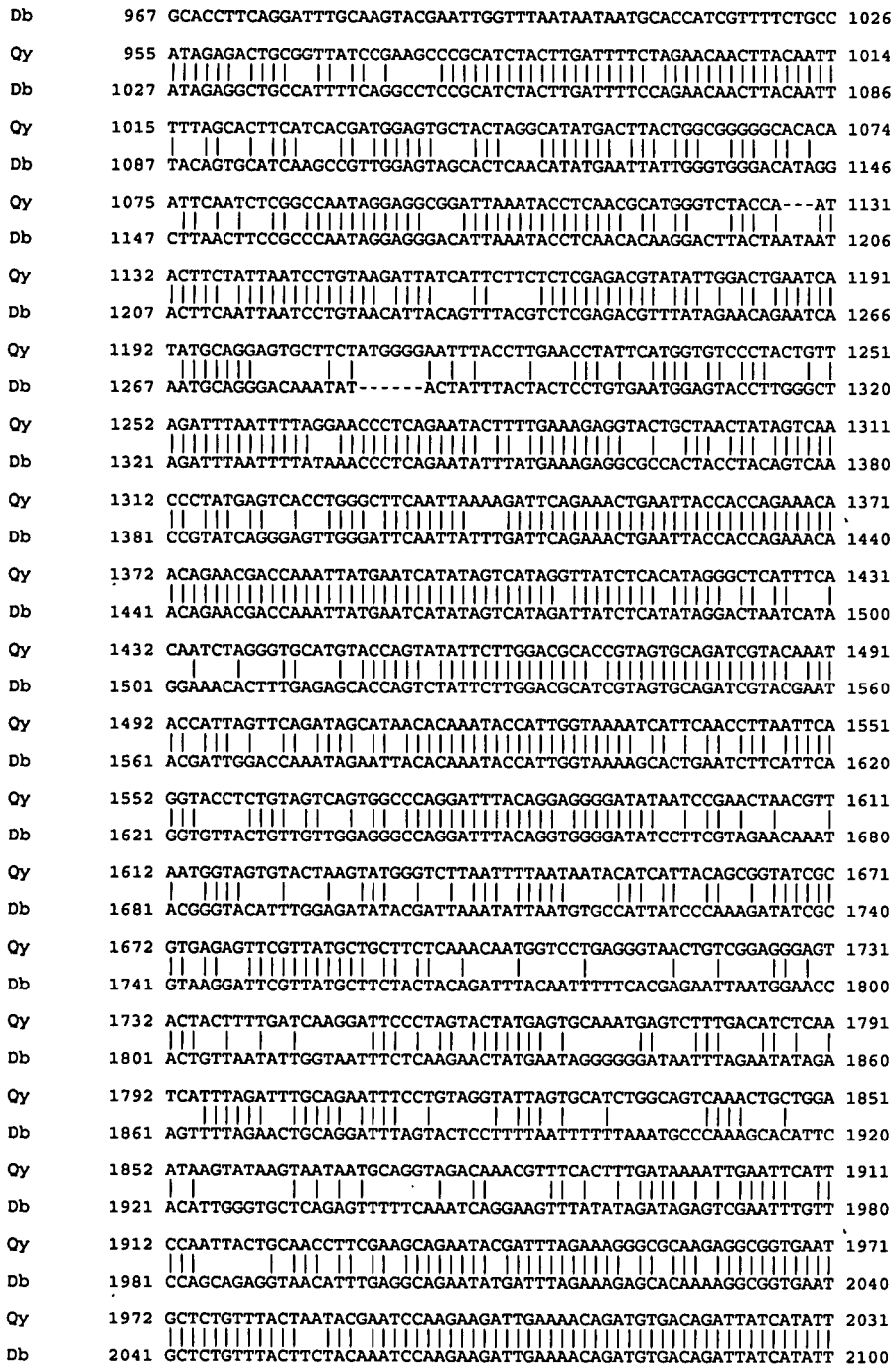
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Db 2401 GAGTGTTATCCAAATTATTTATATCAAAAAATAGGAGAGTCAGAATTAAAAGCTTATACG 2460
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Db 2521 TACAATGCAAAGCATGAAACATTGGATGTTCCAGGTACCGATTCCCTATGGCCGCTTTCA 2580
Qy 2512 GTTGAAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTTTGAATGG 2571
Db 2581 GTTGAAAGCCCAATCGGAAGGTGCGGAGAACCAAATCGATGCGCACCACATTTTGAATGG 2640
Qy 2572 AATCCTGATCTAGATTGTTCCTGCAGAGATGGAGAAAAATGTGCGCATCATTCCCATCAT 2631
Db 2641 AATCCTGATCTAGATTGTTCCTGCAGAGATGGAGAAAGATGTGCGCATCATTCCCATCAT 2700
Qy 2632 TTCTCTTTGGATATTGATATTGGATGCACAGACTTGCATGAGAATCTAGGCGTGTGGGTG 2691
Db 2701 TTCACTTTGGATATTGATGTTGGGTGCACAGACTTGCATGAGAACCTAGGCGTGTGGGTG 2760
Qy 2692 GTATTCAAGATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAATCTGGAATTTATTGAA 2751
Db 2761 GTATTCAAGATTAAGACGCAGGAAGGTTATGCAAGATTAGGAAATCTGGAATTTATCGAA 2820
Qy 2752 GAGAAACCATTATTAGGAGAAGCACTGTCTCGTGTGAAGAGAGCAGAGAAAAAATGGAGA 2811
Db 2821 GAGAAACCATTAATTGGAGAAGCACTGTCTCGTGTGAAGAGAGCGGAAAAAAAATGGAGA 2880
Qy 2812 GACAAACGTGAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAGAAGCT 2871
Db 2881 GACAAACGGGAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAGAAGCT 2940
Qy 2872 GTGGATGCTTTATTTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTGGC 2931
Db 2941 GTGGATGCTTTATTCGTAGATTCTCAATATGATCAATTACAAGCGGATACAAACATTGGC 3000
Qy 2932 ATGATTCATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCTTATCTGTCAGAATTA 2991
Db 3001 ATGATTCATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCGTATCTTTCAGAATTA 3060
Qy 2992 TCTGTTATCCCGGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCGCATTATCACT 3051
Db 3061 CCTGTTATCCCAGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCACATTATCACT 3120
Qy 3052 GCAATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTA 3111
Db 3121 GCAATGTCCTTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTA 3180

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Qy       3112 GCATGCTGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCCTT 3171
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Db       3181 ACATGTTGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCATCGTTCTGACCTT 3240

Qy       3172 GTTATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGC 3231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GTTATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGC 3300

Qy       3232 TATATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGTTGTGTAACGATCCAT 3291
             |||||||| ||||||||||||||||||||||||||||||| || ||||||||||||
Db       3301 TATATCCTTCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGCTGCGTAACGATCCAT 3360

Qy       3292 GAAATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTAT 3351
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GAAATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTAT 3420

Qy       3352 CCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGTATGTAAT 3411
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       3421 CCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGCATGTAAT 3480

Qy       3412 TCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTAC 3471
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 TCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTAC 3540

Qy       3472 AAACCGACTTATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGTGAATAT 3531
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 AAACCGACTTATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGTGAATAT 3600

Qy       3532 GACAGAGGGTATGTGAATTATCCACCACTACCAGCTGGTTATATGACAAAAGAATTAGAA 3591
             |||||||||||||||||||||||||| |||||||||||||| ||||||||||||||||||
Db       3601 GACAGAGGGTATGTGAATTATCCACCAGTACCAGCTGGTTATGTGACAAAAGAATTAGAA 3660

Qy       3592 TACTTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGGGAAGTTTATT 3651
             ||||||||||||||| |||| ||||||||||||||||||||||||||||||||| |||||||||
Db       3661 TACTTCCCAGAAACAGATACAGTATGGATTGAGATTGGAGAAACGGAAGGAAAGTTTATT 3720

Qy       3652 GTAGACAGCGTGGAATTACTCCTTATGGAGGAATAG 3687
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Db       3721 GTAGATAGCGTGGAACTACTCCTCATGGAAGAATAG 3756


RESULT 11
US-08-040-751-4
; Sequence 4, Application US/08040751
; Patent No. 5407825
;  GENERAL INFORMATION:
;    APPLICANT:  Payne, Jewel M
;    APPLICANT:  Sick, August J
;    TITLE OF INVENTION:  No. 5407825el Bacillus thuringiensis isolates
;    TITLE OF INVENTION:  active against Lepidopteran Pests and Genes Encoding No. 54078
;    TITLE OF INVENTION:  Lepidopteran-active Toxins
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID R. SALIWANCHIK
;      STREET:  2421 N.W. 41st STREET, SUITE A-1
;      CITY:  GAINESVILLE
;      STATE:  FL
;      COUNTRY:  USA
;      ZIP:  32606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/040,751
;      FILING DATE:  19930329
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SALIWANCHIK, DAVID R.
;      REFERENCE/DOCKET NUMBER:  MA39.C1.D3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  904-375-8100
;      TELEFAX:  904-372-5800
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3522 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Bacillus thuringiensis
;      STRAIN:  aizawai
;      INDIVIDUAL ISOLATE:  PS81A2
;    IMMEDIATE SOURCE:
;      LIBRARY:  Lambdagem - 11 (tm) Library of August Sick
;      CLONE:  81A2
US-08-040-751-4

  Query Match            48.6%;  Score 1793.4;  DB 1;  Length 3522;
  Best Local Similarity  71.9%;  Pred. No. 0;
  Matches 2497;  Conservative    0;  Mismatches  861;  Indels  117;  Gaps    7;

Qy        228 ACAAATAGCTAGTTTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCA 287
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Db        147 ACTAGGGGATTTTATACTTGGCTTGTTTGATGTAATATGGGGGGCTATAGGTCCTTCACA 206

Qy        288 GTGGGAAATTTTCCTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGC 347
              ||||| || ||  |||| ||  | || | | | ||    |||  ||||   |||    ||
Db        207 ATGGGATATATTTTTAGAGCAAATTGAGCTATTGATCGGCCAAAGAATAGAGGAATTCGC 266

Qy        348 TAGGAATACGGCACTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACA 407
              |||||||  |||| || || |||||||||| || |  ||   |   ||   ||  | |
Db        267 TAGGAATCAGGCAATTTCTAGATTACAAGGGCTAAGCAATCTTTACCGAATTTACACAAA 326

Qy        408 GTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATAC 467
              |  || || | |||  || | | | |  | || ||  |  |||   |   |   ||
Db        327 TGCTTTTAAAAACTGGGAAGTAGATCCTACTAATCCAGCATTAAGAGAAGAGATGCGTAT 386

Qy        468 CCAATATATAGCCTTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAA 527
              |||| ||  | | |  |  || | ||  |  || || || |||||  || ||  |
Db        387 TCAATTTAATGACATGAACAGTGCTCTTACAACAGCTATTCCTCTTTTTTCAGTTCAAGG 446

Qy        528 CCAAGAAGTTCCATTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATT 587
              | ||| ||||  | |||   ||||||| |||||||||||||||||||  |||   | ||
Db        447 TTATGAAATTCCTCTTTTATCAGTATATGTTCAAGCTGCAAATTTACATTTATCGGTTTT 506

Qy        588 GAGAGATGCCTCTCTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTA 647
              ||||||||  ||  | |||||        |  ||  ||             |||  |  ||
Db        507 GAGAGATGTTTCAGTGTTTGGACAACGTTGGGGATTTGATGTAGCAACAATCAATAGTCG 566

Qy        648 TTATGAGCGCCAAGTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAA 707
              |||| |      |     |  |  | || ||| | || |||   |||  ||||||||
Db        567 TTATAATGATTTAACTAGGCTTATTGGCGAATATACTGATTATGCTGTACGTTGGTATAA 626

Qy        708 TACAGGTCTAAATAGCTTGAGAGGGACAAATGCCG---CAAGTTGGGTGCGTTATAATCA 764
              ||| ||  ||||| | ||   | | |   | |  |     | | ||||   | | ||||
Db        627 TACGGGGTTAAATCGTTTACCACGTAATGAAGGGGTACGAGGATGGGCAAGATTTAATAG 686

Qy        765 ATTCCGTAGAGATCTAACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGA 824
              ||  | |||||  ||||  ||   |||||||| | |  |  | |||| ||  || ||
Db        687 GTTTAGAAGAGAGTTAACAATATCAGTATTAGATATTATTTCTTTTTTCCAAAATTACGA 746

Qy        825 CACTCGCACTTATCCAATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGC 884
              || |    ||||||||    || |    ||| |||||  ||||||| ||||||||  |
Db        747 TTCTAGATTATATCCAATTCCGACAATCTATCAATTAACGCGGGAAGTATATACAGATCC 806

Qy        885 AATTGGAGCAACAGGGGTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTC 944
                                      || || ||  |      || |||    | | ||
Db        807 ----------------------GGTAATTAATATAACTGATTATAGAGTTACCCCAAG 842

Qy        945 GTTTTCCGCTATAGAGACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACA 1004
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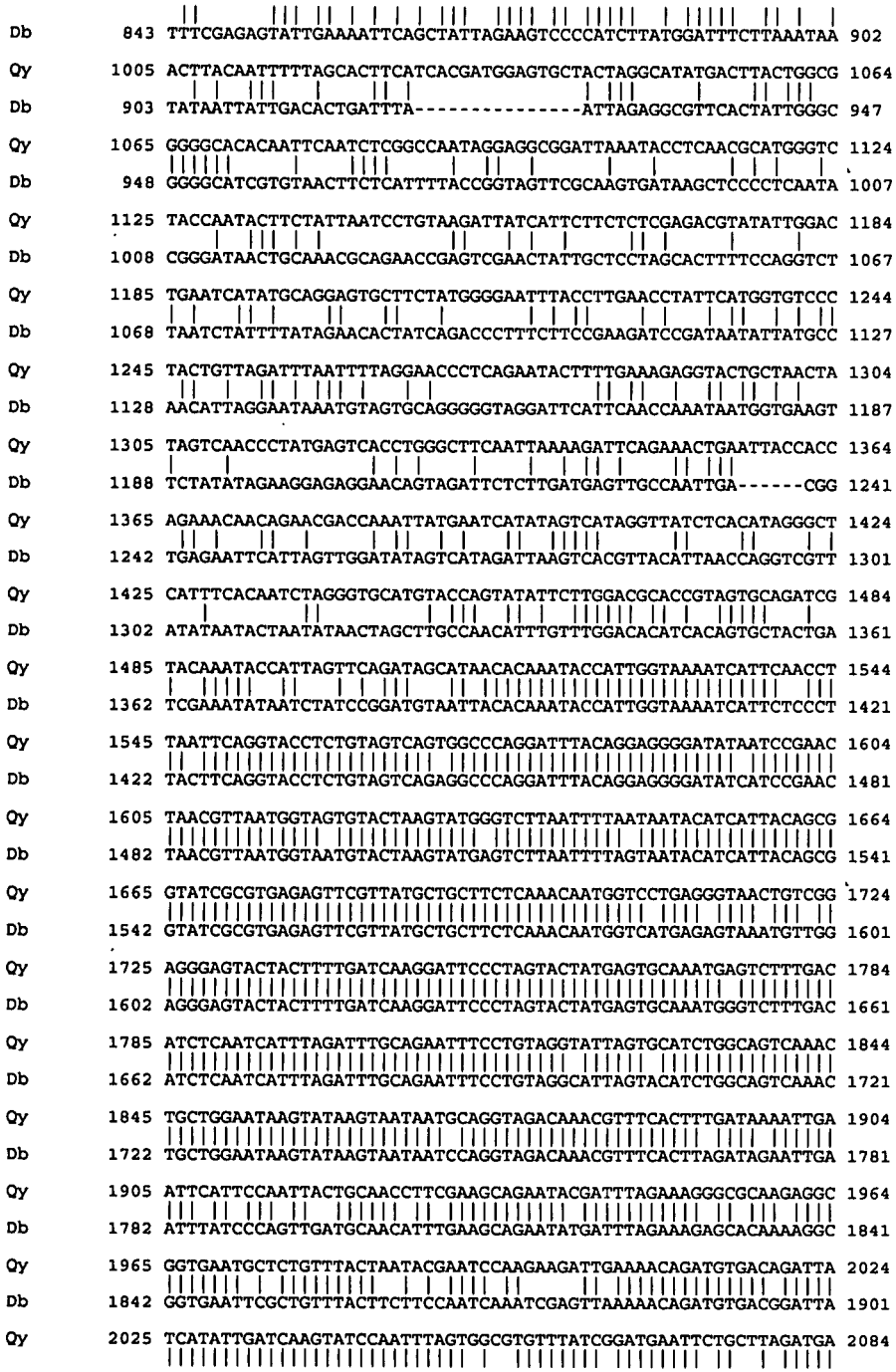
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Db 903 TATAATTATTGACACTGATTTA----------ATTAGAGGCGTTCACTATTGGGC 947
Qy 1065 GGGGCACACAATTCAATCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGTC 1124
Db 948 GGGGCATCGTGTAACTTCTCATTTTACCGGTAGTTCGCAAGTGATAAGCTCCCCTCAATA 1007
Qy 1125 TACCAATACTTCTATTAATCCTGTAAGATTATCATTCTTCTCTCGAGACGTATATTGGAC 1184
Db 1008 CGGGATAACTGCAAACGCAGAACCGAGTCGAACTATTGCTCCTAGCACTTTTCCAGGTCT 1067
Qy 1185 TGAATCATATGCAGGAGTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCC 1244
Db 1068 TAATCTATTTTATAGAACACTATCAGACCCTTTCTTCCGAAGATCCGATAATATTATGCC 1127
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Qy 1305 TAGTCAACCCTATGAGTCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACC 1364
Db 1188 TCTATATAGAAGGAGAGGAACAGTAGATTCTCTTGATGAGTTGCCAATTGA------CGG 1241
Qy 1365 AGAAACAACAGAACGACCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCT 1424
Db 1242 TGAGAATTCATTAGTTGGATATAGTCATAGATTAAGTCACGTTACATTAACCAGGTCGTT 1301
Qy 1425 CATTTCACAATCTAGGGTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGATCG 1484
Db 1302 ATATAATACTAATATAACTAGCTTGCCAACATTTGTTTGGACACATCACAGTGCTACTGA 1361
Qy 1485 TACAAATACCATTAGTTCAGATAGCATAACACAAATACCATTGGTAAAATCATTCAACCT 1544
Db 1362 TCGAAATATAATCTATCCGGATGTAATTACACAAATACCATTGGTAAAATCATTCTCCCT 1421
Qy 1545 TAATTCAGGTACCTCTGTAGTCAGTGGCCCAGGATTTACAGGAGGGGATATAATCCGAAC 1604
Db 1422 TACTTCAGGTACCTCTGTAGTCAGAGGCCCAGGATTTACAGGAGGGGATATCATCCGAAC 1481
Qy 1605 TAACGTTAATGGTAGTGTACTAAGTATGGGTCTTAATTTTAATAATACATCATTACAGCG 1664
Db 1482 TAACGTTAATGGTAATGTACTAAGTATGAGTCTTAATTTTAGTAATACATCATTACAGCG 1541
Qy 1665 GTATCGCGTGAGAGTTCGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGTCGG 1724
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Qy 1725 AGGGAGTACTACTTTTGATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGAC 1784
Db 1602 AGGGAGTACTACTTTTGATCAAGGATTCCCTAGTACTATGAGTGCAAATGGGTCTTTGAC 1661
Qy 1785 ATCTCAATCATTTAGATTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAAAC 1844
Db 1662 ATCTCAATCATTTAGATTTGCAGAATTTCCTGTAGGCATTAGTACATCTGGCAGTCAAAC 1721
Qy 1845 TGCTGGAATAAGTATAAGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATTGA 1904
Db 1722 TGCTGGAATAAGTATAAGTAATAATCCAGGTAGACAAACGTTTCACTTAGATAGAATTGA 1781
Qy 1905 ATTCATTCCAATTACTGCAACCTTCGAAGCAGAATACGATTTAGAAAGGGCGCAAGAGGC 1964
Db 1782 ATTTATCCCAGTTGATGCAACATTTGAAGCAGAATATGATTTAGAAAGAGCACAAAAGGC 1841
Qy 1965 GGTGAATGCTCTGTTTACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTA 2024
Db 1842 GGTGAATTCGCTGTTTACTTCTTCCAATCAAATCGAGTTAAAAACAGATGTGACGGATTA 1901
Qy 2025 TCATATTGATCAAGTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGA 2084
Db 1902 TCATATTGATCAAGTATCCAATTTAGTAGATTGTTTATCCGATGAATTTTGTCTGGATGA 1961
Qy 2085 AAAGAGAGAATTACTTGAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAACTT 2144
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Qy 2145 ACTCCAAGATCCAAACTTCACATCCATCAATAAGCAACCAGACTTCATATCTACTAATGA 2204
Db 2022 ACTTCAAGATCCAAACTTCAGAGGGATCAATAGGCAACCAGAC---------- 2064
Qy 2205 GCAATCGAATTTCACATCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAA 2264
Db 2065 ----------CGTGGCTGGAGAGGAAGTACGGA 2087
Qy 2265 CATTACAATCCAGGAAGGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGAC 2324
Db 2088 TATTACCATCCAAGGAGGAGATGACGTATTCAAAGAGAATTACGTCACACTACCAGGTAC 2147
Qy 2325 TTTTAATGAGTGTTATCCGACGTATTTATATCAAAAAATAGGAGAGTCGGAATTAAAAGC 2384
Db 2148 CTTTGATGAGTGCTATCCAACGTATTTGTATCAAAAAATAGATGAGTCGAAATTAAAAGC 2207
Qy 2385 TTATACTCGCTACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTT 2444
Db 2208 CTATAACCGTTACCAATTAAGAGGGTATATCGAAGATAGTCAAGACTTAGAAATCTATTT 2267
Qy 2445 GATTCGTTATAATGCGAAACATGAAACATTGGATGTTCCAGGTACCGAGTCCGTATGGCC 2504
Db 2268 AATTCGCTACAATGCAAAACACGAAACAGTAAATGTACCAGGTACGGGTTCCTTATGGCC 2327
Qy 2505 GCTTTCAGTTGAAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTT 2564
Db 2328 GCTTTCAGTCGAAAGTCCAATTGGAAGGTGTGGAGAACCGAATCGGTGTGTGCCACACCT 2387
Qy 2565 TGAATGGAATCCTGATCTAGATTGTTCCTGCAGAGATGGAGAAAAATGTGCGCATCATTC 2624
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Qy 2625 CCATCATTTCTCTTTGGATATTGATATTGGATGCACAGACTTGCATGAGAATCTAGGCGT 2684
Db 2448 CCATCATTTCTCCTTGGACATTGATGTTGGATGCACAGACTTGCAAGAGGATCTAGGCGT 2507
Qy 2685 GTGGGTGGTATTCAAGATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAATCTGGAATT 2744
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Qy 2745 TATTGAAGAGAAACCATTATTAGGAGAAGCACTGTCTCGTGTGAAGAGAGCAGAGAAAAA 2804
Db 2568 TATCGAAGAGAAACCATTAATTGGAGAAGCACTGTCTCGTGTGAAGAGAGCGGAAAAAAA 2627
Qy 2805 ATGGAGAGACAAACGTGAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAA 2864
Db 2628 ATGGAGAGACAAACGGGAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAA 2687
Qy 2865 AGAAGCTGTGGATGCTTTATTTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAA 2924
Db 2688 AGAAGCTGTGGATGCTTTATTCGTAGATTCTCAATATGATAGATTACAAGCAGATACAAA 2747
Qy 2925 CATTGGCATGATTCATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCTTATCTGTC 2984
Db 2748 CATTGGTATGATTCATGCGGCAGATAGACTTGTTCATCAGATCCACGAGGCTTATCTTCC 2807
Qy 2985 AGAATTATCTGTTATCCCGGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCGCAT 3044
Db 2808 AGAACTACCTTTCATTCCAGGAATAAATGTGGTGATTTTTGAAGAATTAGAAAACCGTAT 2867
Qy 3045 TATCACTGCAATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAA 3104
Db 2868 TTCTACTGCATTATCCCTATATGATGCGAGAAATGTCATTAAAAATGGCGATTTCAATAA 2927
Qy 3105 TGGATTAGCATGCTGGAATGTAAAAGGGCATGTAGAT---GTACAACAGAGCCATCACCG 3161
Db 2928 TGGCTTATCATGCTGGAACGTGAAAGGGCATGTAGATGTAGTAGAACAAAACAACCACCG 2987

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Qy       3162 TTCTGTCCTTGTTATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCC 3221
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Db       2988 TTCGGTCCTTGTTGTCCCGGAATGGGAAGCAGAAGTGTCACAAACAATTCGTGTCTGTCC 3047

Qy       3222 GGGGCGTGGCTATATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGTTGTGT 3281
             |||||||||||||||||||||||| |||||||||||||||||||||||| ||||| ||
Db       3048 GGGGCGTGGCTATATCCTCCGTGTTACAGCGTACAAAGAGGGATATGGAGAAGGTTGCGT 3107

Qy       3282 AACGATCCATGAAATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGA 3341
             ||| |||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       3108 AACCATCCATGAGATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGA 3167

Qy       3342 GGAAGTGTATCCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGC 3401
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Db       3168 GGAAGTGTATCCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGC 3227

Qy       3402 AG------------TATGTAATTCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGA 3449
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Db       3228 AGGATCCACAGATTCATGTAATTCCCGTAATATCAGATATGAGGATGCATATGAAATGAA 3287

Qy       3450 TACTACAGCATCTGTTAATTACAAACCGACTTATGAAGAAGAAACGTATACAGATGTACG 3509
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Db       3288 TACTACAGCATCTGTTAATTACAAACCGACTTACGAAGAAGAAAGGTATACAGATGTACA 3347

Qy       3510 AAGAGATAATCATTGTGAATATGACAGAGGGTATGTGAATTATCCACCACTACCAGCTGG 3569
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Db       3348 AGGAGATAATCATTGTGAATATGACAGAGGGTATGTGAATTATCGACCAGTACCAGCTGG 3407

Qy       3570 TTATATGACAAAAGAATTAGAATACTTCCCAGAAACCGATAAGGTATGGATTGAGATTGG 3629
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Db       3408 TTATGTGACAAAAGAATTAGAGTACTTCCCAGAAACCGATAAGGTATGGATTGAGATCGG 3467

Qy       3630 AGAAACGGAAGGGAAGTTTATTGTAGACAGCGTGGAATTACTCCTTATGGAGGAA 3684
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Db       3468 AGAAACGGAAGGGAAGTTTATTGTAGACAATGTCGAATTACTCCTTATGGAGGAA 3522
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RESULT 12
US-08-291-368-1
; Sequence 1, Application US/08291368
; Patent No. 5686069
;  GENERAL INFORMATION:
;    APPLICANT:  Payne, Jewel M.
;    APPLICANT:  Sick, August J.
;    TITLE OF INVENTION:  No. 5686069el Bacillus thuringiensis Isolates
;    TITLE OF INVENTION:  Active Against Lepidopteran Pests
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Saliwanchik & Saliwanchik
;      STREET:  2421 N.W. 41st Street, Suite A-1
;      CITY:  Gainesville
;      STATE:  FL
;      COUNTRY:  US
;      ZIP:  32606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/291,368
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/597,607
;      FILING DATE:  15-OCT-90
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Saliwanchik, David R.
;      REGISTRATION NUMBER:  31,794
;      REFERENCE/DOCKET NUMBER:  MA50.C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (904)375-8100
;      TELEFAX:  (904)372-5800
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3522 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Bacillus thuringiensis
;      STRAIN:  aizawai
;      INDIVIDUAL ISOLATE:  PS81A2
;    IMMEDIATE SOURCE:
;      LIBRARY:  Lambdagem - 11 (tm) Library of August Sick
;      CLONE:  81A2
US-08-291-368-1

  Query Match            48.6%;  Score 1793.4;  DB 1;  Length 3522;
  Best Local Similarity  71.9%;  Pred. No. 0;
  Matches 2497;  Conservative    0;  Mismatches  861;  Indels  117;  Gaps    7;
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Qy        228 ACAAATAGCTAGTTTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCA 287
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Db        147 ACTAGGGGATTTTATACTTGGCTTGTTTGATGTAATATGGGGGGCTATAGGTCCTTCACA 206

Qy        288 GTGGGAAATTTTCCTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGC 347
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Db        207 ATGGGATATATTTTTAGAGCAAATTGAGCTATTGATCGGCCAAAGAATAGAGGAATTCGC 266

Qy        348 TAGGAATACGGCACTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACA 407
              |||||||  |||| || || |||||||||| || |  ||    |  ||  ||   | |
Db        267 TAGGAATCAGGCAATTTCTAGATTACAAGGGCTAAGCAATCTTTACCGAATTTACACAAA 326

Qy        408 GTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATAC 467
              |  || || | |||  || | | | |  | || ||  |   |||   |   |   ||
Db        327 TGCTTTTAAAAACTGGGAAGTAGATCCTACTAATCCAGCATTAAGAGAAGAGATGCGTAT 386

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Db        387 TCAATTTAATGACATGAACAGTGCTCTTACAACAGCTATTCCTCTTTTTTCAGTTCAAGG 446

Qy        528 CCAAGAAGTTCCATTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATT 587
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Db        447 TTATGAAATTCCTCTTTTATCAGTATATGTTCAAGCTGCAAATTTACATTTATCGGTTTT 506

Qy        588 GAGAGATGCCTCTCTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTA 647
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Db        507 GAGAGATGTTTCAGTGTTTGGACAACGTTGGGGATTTGATGTAGCAACAATCAATAGTCG 566

Qy        648 TTATGAGCGCCAAGTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAA 707
              |||| |      |      |  |   | || ||| | || |||   |||   ||||||||
Db        567 TTATAATGATTTAACTAGGCTTATTGGCGAATATACTGATTATGCTGTACGTTGGTATAA 626

Qy        708 TACAGGTCTAAATAGCTTGAGAGGGACAAATGCCG---CAAGTTGGGTGCGTTATAATCA 764
              ||| ||  ||||| | ||   | | |   | |  |     | | ||||   | | ||||
Db        627 TACGGGGTTAAATCGTTTACCACGTAATGAAGGGGTACGAGGATGGGCAAGATTTAATAG 686

Qy        765 ATTCCGTAGAGATCTAACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGA 824
              ||  | |||||  ||||  ||   |||||||| | |  |  | |||| ||  || ||
Db        687 GTTTAGAAGAGAGTTAACAATATCAGTATTAGATATTATTTCTTTTTTCCAAAATTACGA 746

Qy        825 CACTCGCACTTATCCAATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGC 884
              || |    ||||||||    || |    ||| |||||  ||||||| ||||||||  |
Db        747 TTCTAGATTATATCCAATTCCGACAATCTATCAATTAACGCGGGAAGTATATACAGATCC 806

Qy        885 AATTGGAGCAACAGGGGTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTC 944
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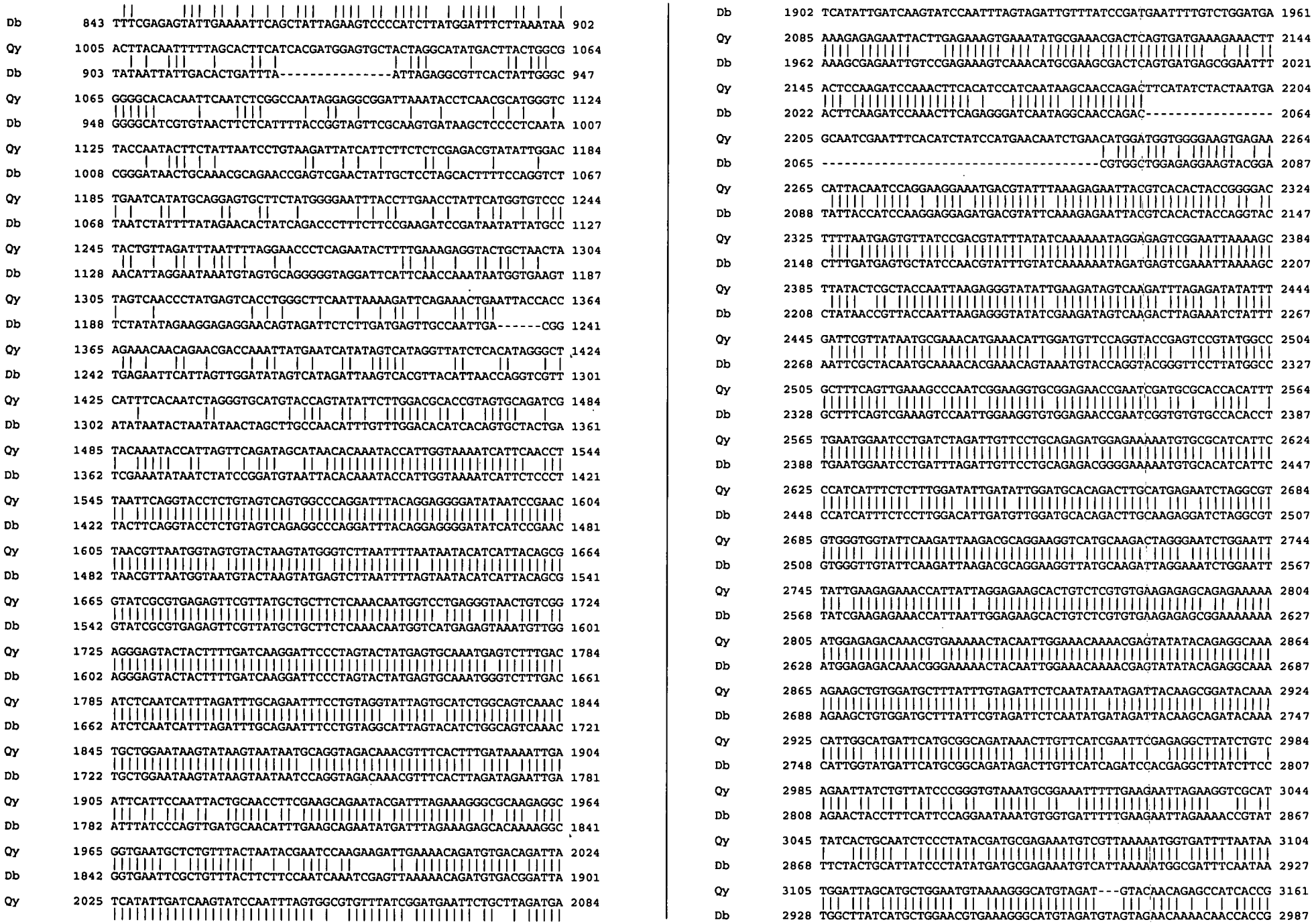

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Db       2988 TTCGGTCCTTGTTGTCCCGGAATGGGAAGCAGAAGTGTCACAAACAATTCGTGTCTGTCC 3047

Qy       3222 GGGGCGTGGCTATATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGTTGTGT 3281
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Db       3048 GGGGCGTGGCTATATCCTCCGTGTTACAGCGTACAAAGAGGGATATGGAGAAGGTTGCGT 3107

Qy       3282 AACGATCCATGAAATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGA 3341
             ||| |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       3108 AACCATCCATGAGATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGA 3167

Qy       3342 GGAAGTGTATCCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGC 3401
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Qy       3402 AG------------TATGTAATTCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGA 3449
              ||              |||||||||||||||    ||||||||||||||||||| |   |
Db       3228 AGGATCCACAGATTCATGTAATTCCCGTAATATCAGATATGAGGATGCATATGAAATGAA 3287

Qy       3450 TACTACAGCATCTGTTAATTACAAACCGACTTATGAAGAAGAAACGTATACAGATGTACG 3509
             |||||||||||||||||||||||||||||| |||||||||| ||||||||||||||||
Db       3288 TACTACAGCATCTGTTAATTACAAACCGACTTACGAAGAAGAAAGGTATACAGATGTACA 3347

Qy       3510 AAGAGATAATCATTGTGAATATGACAGAGGGTATGTGAATTATCCACCACTACCAGCTGG 3569
             | |||||||||||||||||||||||||||||||||||||||||||| |||| ||||||||||
Db       3348 AGGAGATAATCATTGTGAATATGACAGAGGGTATGTGAATTATCGACCAGTACCAGCTGG 3407

Qy       3570 TTATATGACAAAAGAATTAGAATACTTCCCAGAAACCGATAAGGTATGGATTGAGATTGG 3629
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Qy       3630 AGAAACGGAAGGGAAGTTTATTGTAGACAGCGTGGAATTACTCCTTATGGAGGAA 3684
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Db       3468 AGAAACGGAAGGGAAGTTTATTGTAGACAATGTCGAATTACTCCTTATGGAGGAA 3522


RESULT 13
US-08-962-190-1
; Sequence 1, Application US/08962190
; Patent No. 5985267
;  GENERAL INFORMATION:
;    APPLICANT:  Payne, Jewel M.
;    APPLICANT:  Sick, August J.
;    TITLE OF INVENTION:  No. 5985267el Bacillus thuringiensis Isolates
;    TITLE OF INVENTION:  Active Against Lepidopteran Pests
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Saliwanchik & Saliwanchik
;      STREET:  2421 N.W. 41st Street, Suite A-1
;      CITY:  Gainesville
;      STATE:  FL
;      COUNTRY:  US
;      ZIP:  32606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/962,190
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/291,368
;      FILING DATE:
;      APPLICATION NUMBER:  07/597,607
;      FILING DATE:  15-OCT-90
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Saliwanchik, David R.
;      REGISTRATION NUMBER:  31,794
;      REFERENCE/DOCKET NUMBER:  MA50.C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (904)375-8100
;      TELEFAX:  (904)372-5800
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3522 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Bacillus thuringiensis
;      STRAIN:  aizawai
;      INDIVIDUAL ISOLATE:  PS81A2
;    IMMEDIATE SOURCE:
;      LIBRARY:  Lambdagem - 11 (tm) Library of August Sick
;      CLONE:  81A2
US-08-962-190-1

  Query Match             48.6%;  Score 1793.4;  DB 2;  Length 3522;
  Best Local Similarity   71.9%;  Pred. No. 0;
  Matches 2497;  Conservative    0;  Mismatches  861;  Indels  117;  Gaps    7;

Qy        228 ACAAATAGCTAGTTTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCA 287
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Db        147 ACTAGGGGATTTTATACTTGGCTTGTTTGATGTAATATGGGGGGCTATAGGTCCTTCACA 206

Qy        288 GTGGGAAATTTTCCTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGC 347
              ||||| || ||  |||| ||  | || | | | ||    |||  ||||  |||   ||
Db        207 ATGGGATATATTTTTAGAGCAAATTGAGCTATTGATCGGCCAAAGAATAGAGGAATTCGC 266

Qy        348 TAGGAATACGGCACTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACA 407
              |||||||  |||| || || ||||||||||  || |  ||   |   ||  ||   | |
Db        267 TAGGAATCAGGCAATTTCTAGATTACAAGGGCTAAGCAATCTTTACCGAATTTACACAAA 326

Qy        408 GTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATAC 467
              |  || || | |||  || | | | |  | || ||  |  |||   |  |   ||
Db        327 TGCTTTTAAAAACTGGGAAGTAGATCCTACTAATCCAGCATTAAGAGAAGAGATGCGTAT 386

Qy        468 CCAATATATAGCCTTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAA 527
              |||| ||  | | |  |   || | ||   |  || || || |||||  || ||  |
Db        387 TCAATTTAATGACATGAACAGTGCTCTTACAACAGCTATTCCTCTTTTTTCAGTTCAAGG 446

Qy        528 CCAAGAAGTTCCATTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATT 587
              | ||| ||||  | |||   ||||||| ||||||||||||||||||  |||   | ||
Db        447 TTATGAAATTCCTCTTTTATCAGTATATGTTCAAGCTGCAAATTTACATTTATCGGTTTT 506

Qy        588 GAGAGATGCCTCTCTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTA 647
              ||||||||  ||  | |||||       |  ||  ||          |||  |  ||
Db        507 GAGAGATGTTTCAGTGTTTGGACAACGTTGGGGATTTGATGTAGCAACAATCAATAGTCG 566

Qy        648 TTATGAGCGCCAAGTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAA 707
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Qy        708 TACAGGTCTAAATAGCTTGAGAGGGACAAATGCCG---CAAGTTGGGTGCGTTATAATCA 764
              ||| ||  ||||| | ||   | | |   | | |    | | ||||   | | ||||
Db        627 TACGGGGTTAAATCGTTTACCACGTAATGAAGGGGTACGAGGATGGGCAAGATTTAATAG 686

Qy        765 ATTCCGTAGAGATCTAACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGA 824
              ||  | |||||  ||||  ||   |||||||| |  |  |  | |||| ||  || ||
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Qy        825 CACTCGCACTTATCCAATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGC 884
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Db        747 TTCTAGATTATATCCAATTCCGACAATCTATCAATTAACGCGGGAAGTATATACAGATCC 806

Qy        885 AATTGGAGCAACAGGGGTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTC 944
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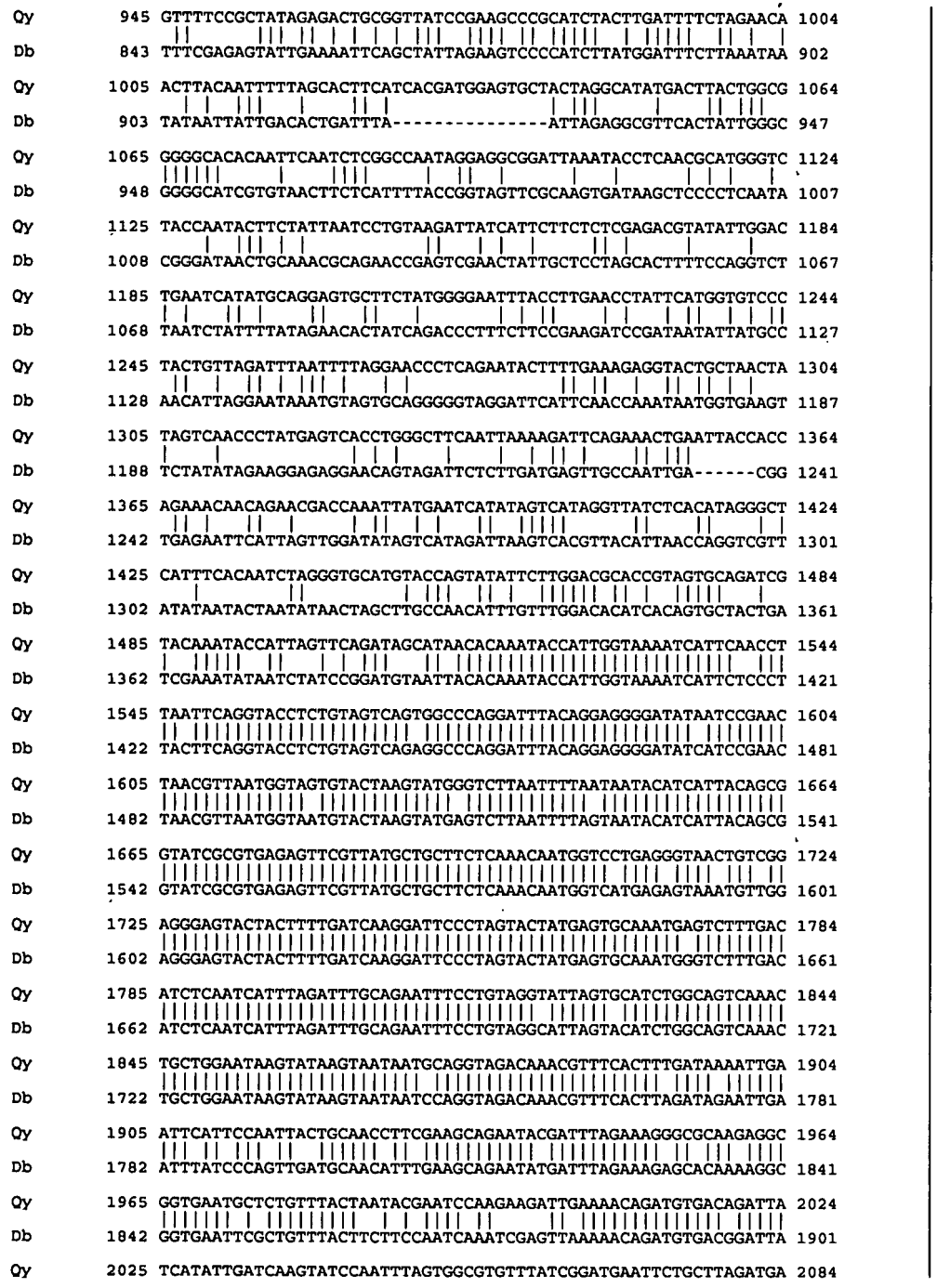

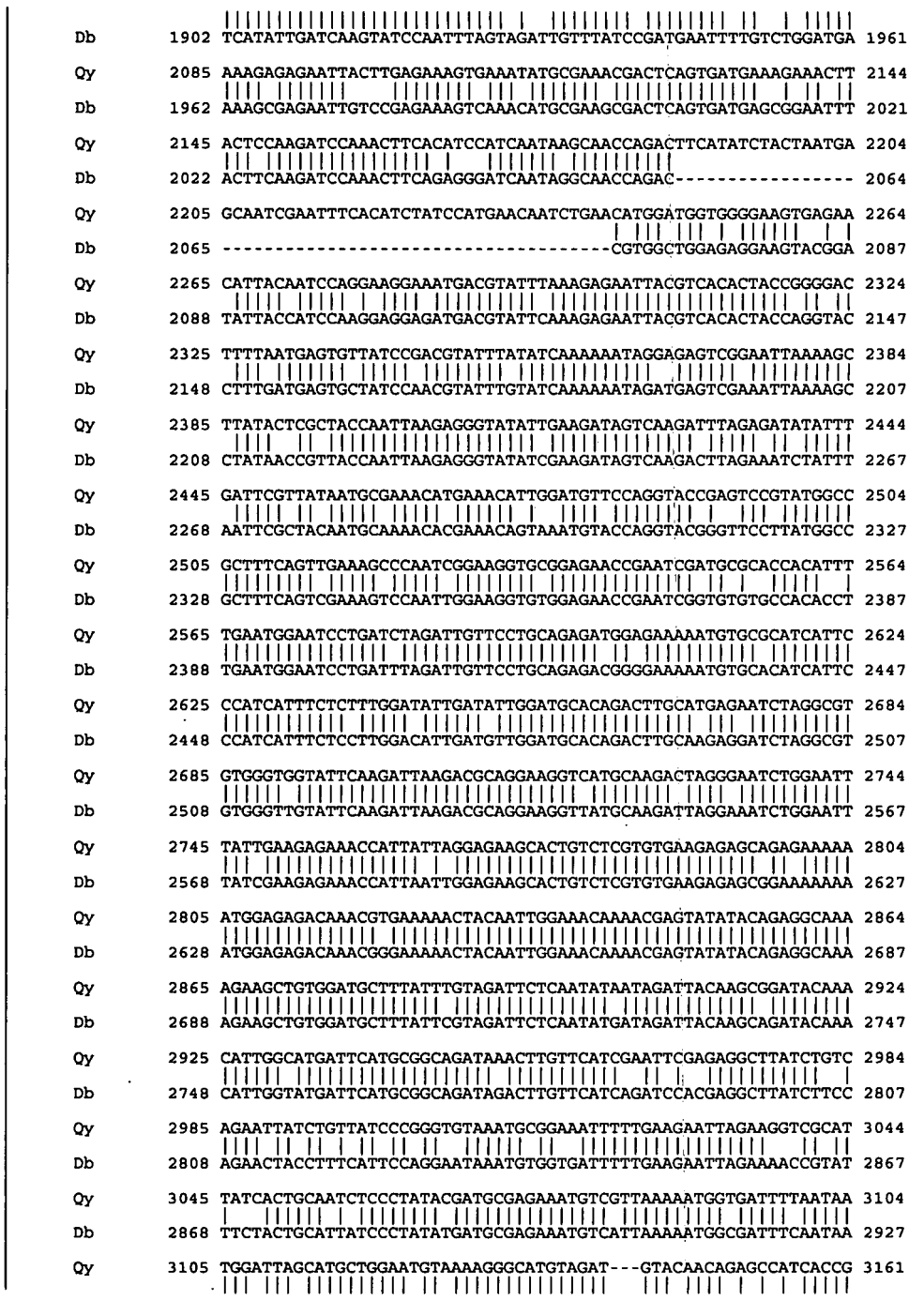

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              ||| ||||||||| |||| ||||||||||||||||||||||| || |||| ||||||||
Db       2988 TTCGGTCCTTGTTGTCCCGGAATGGGAAGCAGAAGTGTCACAAACAATTCGTGTCTGTCC 3047

Qy       3222 GGGGCGTGGCTATATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGTTGTGT 3281
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Db       3048 GGGGCGTGGCTATATCCTCCGTGTTACAGCGTACAAAGAGGGATATGGAGAAGGTTGCGT 3107

Qy       3282 AACGATCCATGAAATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGA 3341
              ||| |||||||| ||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3342 GGAAGTGTATCCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGC 3401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3402 AG------------TATGTAATTCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGA 3449
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Db       3288 TACTACAGCATCTGTTAATTACAAACCGACTTACGAAGAAGAAAGGTATACAGATGTACA 3347

Qy       3510 AAGAGATAATCATTGTGAATATGACAGAGGGTATGTGAATTATCCACCACTACCAGCTGG 3569
              | ||||||||||||||||||||||||||||||||||||||||| |||| ||||||||||
Db       3348 AGGAGATAATCATTGTGAATATGACAGAGGGTATGTGAATTATCGACCAGTACCAGCTGG 3407

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Db       3408 TTATGTGACAAAAGAATTAGAGTACTTCCCAGAAACCGATAAGGTATGGATTGAGATCGG 3467

Qy       3630 AGAAACGGAAGGGAAGTTTATTGTAGACAGCGTGGAATTACTCCTTATGGAGGAA 3684
              |||||||||||||||||||||||||||||  || ||||||||||||||||||||
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RESULT 14
PCT-US95-10310-1
; Sequence 1, Application PC/TUS9510310
;  GENERAL INFORMATION:
;    APPLICANT:  MYCOGEN CORPORATION
;    APPLICANT:  STREET ADDRESS:     5501 Oberlin Drive
;    APPLICANT:  CITY:   San Diego
;    APPLICANT:  STATE/PROVINCE:   California
;    APPLICANT:  COUNTRY:   US
;    APPLICANT:  POSTAL CODE/ZIP:   92121
;    APPLICANT:  PHONE NUMBER:   (619) 453-8030
;    APPLICANT:  FAX NUMBER:   (619) 453-6991
;    TITLE OF INVENTION:  Protein Toxins Active Against Lepidopteran Pests
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Saliwanchik & Saliwanchik
;      STREET:  2421 N.W. 41st Street, Suite A-1
;      CITY:  Gainesville
;      STATE:  FL
;      COUNTRY:  US
;      ZIP:  32606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/10310
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/597,607
;      FILING DATE:  15-OCT-90
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Saliwanchik, David R.
;      REGISTRATION NUMBER:  31,794
;      REFERENCE/DOCKET NUMBER:  MA50.C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (904)375-8100
;      TELEFAX:  (904)372-5800
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3522 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Bacillus thuringiensis
;      STRAIN:  aizawai
;      INDIVIDUAL ISOLATE:  PS81A2
;    IMMEDIATE SOURCE:
;      LIBRARY:  Lambdagem - 11 (tm) Library of August Sick
;      CLONE:  81A2
PCT-US95-10310-1

  Query Match             48.6%;  Score 1793.4;  DB 5;  Length 3522;
  Best Local Similarity   71.9%;  Pred. No. 0;
  Matches 2497;  Conservative    0;  Mismatches  861;  Indels  117;  Gaps    7;

Qy        228 ACAAATAGCTAGTTTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCA 287
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Db        147 ACTAGGGGATTTTATACTTGGCTTGTTTGATGTAATATGGGGGGCTATAGGTCCTTCACA 206

Qy        288 GTGGGAAATTTTCCTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGC 347
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Db        207 ATGGGATATATTTTTAGAGCAAATTGAGCTATTGATCGGCCAAAGAATAGAGGAATTCGC 266

Qy        348 TAGGAATACGGCACTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACA 407
              |||||||  |||| || || ||||||||||  || |  ||   |   ||   ||  | |
Db        267 TAGGAATCAGGCAATTTCTAGATTACAAGGGCTAAGCAATCTTTACCGAATTTACACAAA 326

Qy        408 GTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATAC 467
              |  || || | |||   || | | |  | || ||  |   |||    |   |   ||
Db        327 TGCTTTTAAAAACTGGGAAGTAGATCCTACTAATCCAGCATTAAGAGAAGAGATGCGTAT 386

Qy        468 CCAATATATAGCCTTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAA 527
              |||| ||  | | |  |   || | ||   |  || || || |||||  || ||  |
Db        387 TCAATTTAATGACATGAACAGTGCTCTTACAACAGCTATTCCTCTTTTTTCAGTTCAAGG 446

Qy        528 CCAAGAAGTTCCATTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATT 587
              | ||| |||| | |||   ||||||| ||||||||||||||||||  |||   | ||
Db        447 TTATGAAATTCCTCTTTTATCAGTATATGTTCAAGCTGCAAATTTACATTTATCGGTTTT 506

Qy        588 GAGAGATGCCTCTCTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTA 647
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Db        507 GAGAGATGTTTCAGTGTTTGGACAACGTTGGGGATTTGATGTAGCAACAATCAATAGTCG 566

Qy        648 TTATGAGCGCCAAGTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAA 707
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Db        567 TTATAATGATTTAACTAGGCTTATTGGCGAATATACTGATTATGCTGTACGTTGGTATAA 626

Qy        708 TACAGGTCTAAATAGCTTGAGAGGGACAAATGCCG---CAAGTTGGGTGCGTTATAATCA 764
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Qy        765 ATTCCGTAGAGATCTAACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGA 824
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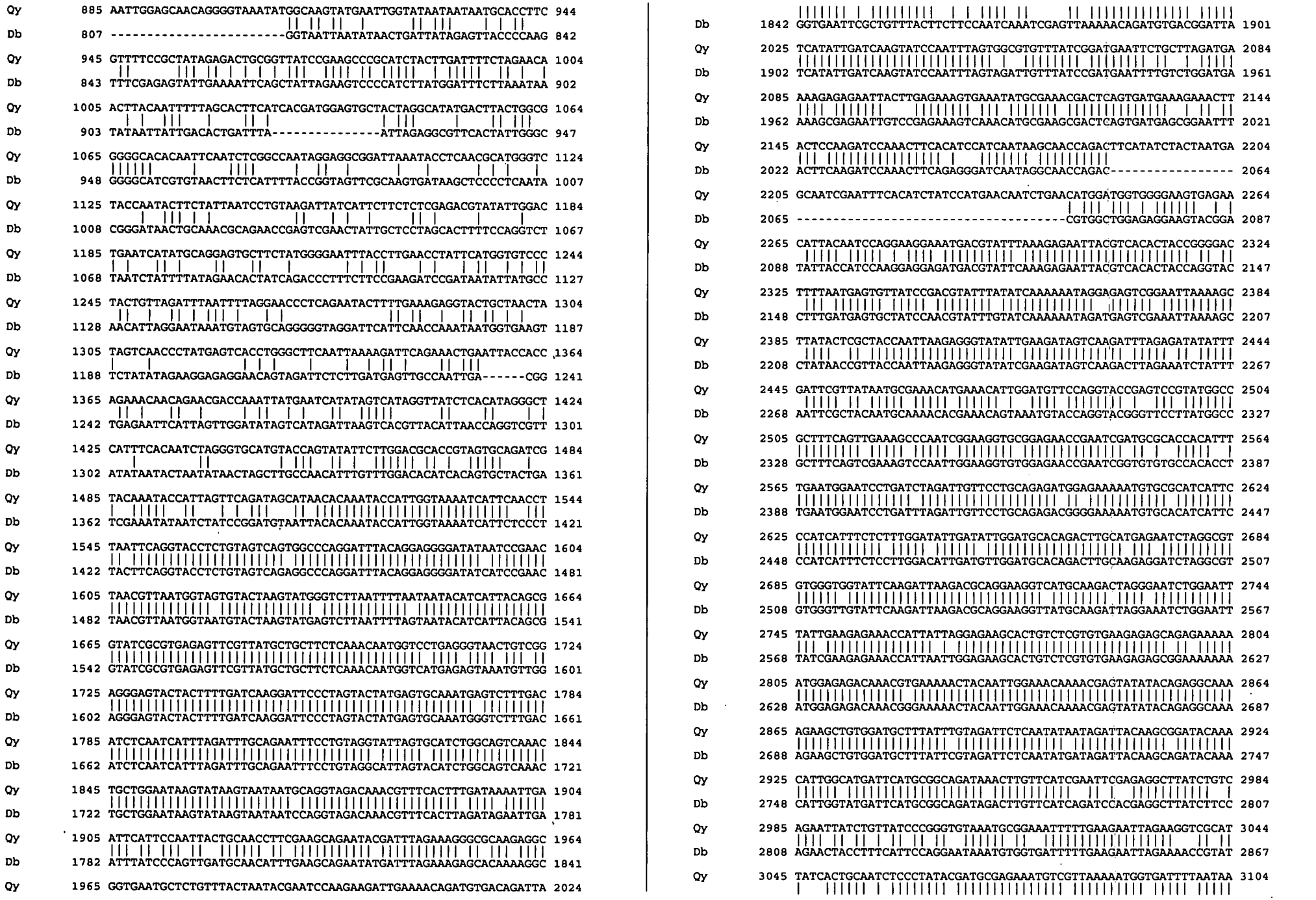
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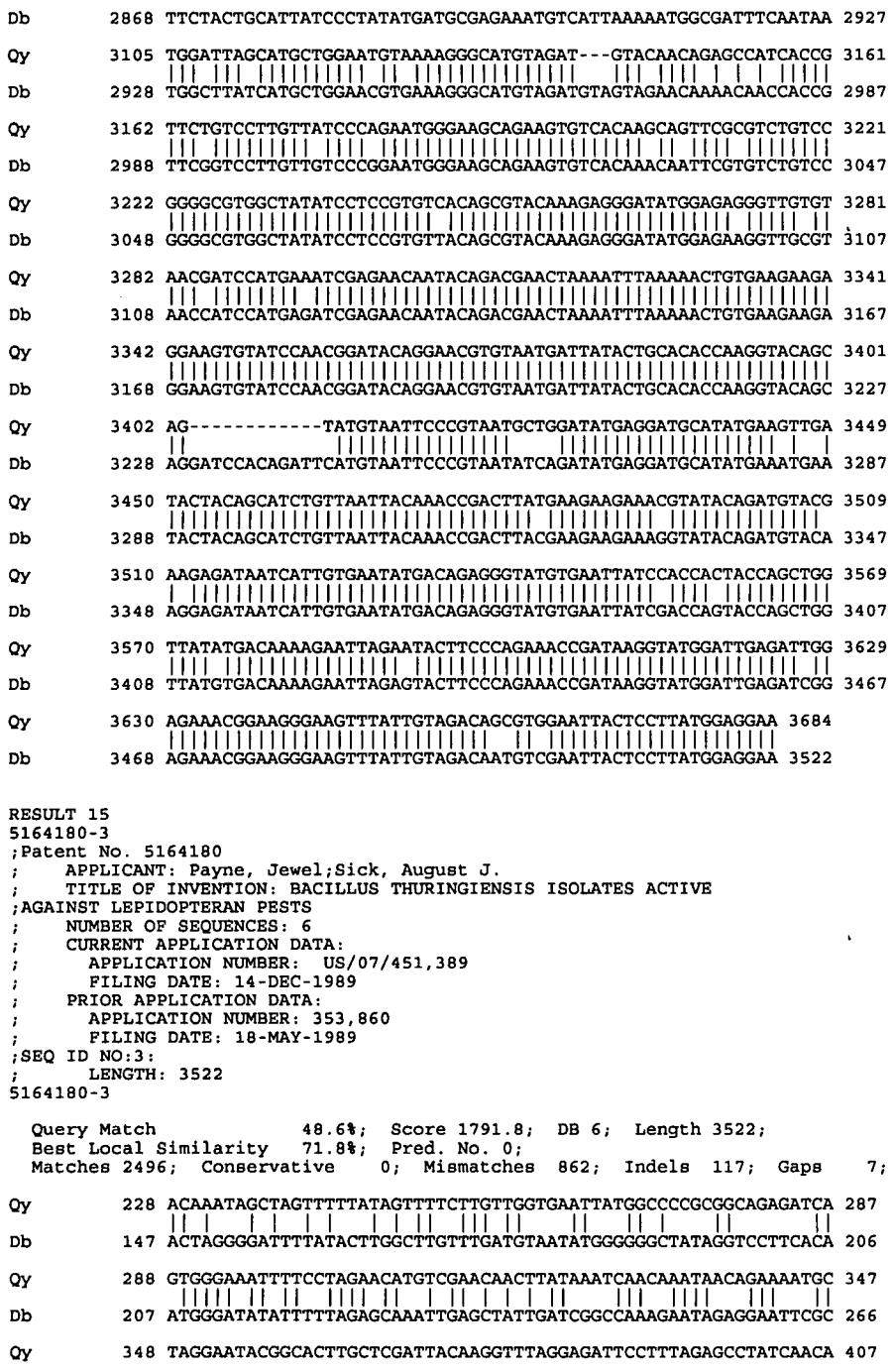

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;AGAINST LEPIDOPTERAN PESTS
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/451,389
; FILING DATE: 14-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 353,860
; FILING DATE: 18-MAY-1989
;SEQ ID NO:3:
; LENGTH: 3522
5164180-3

Query Match 48.6%; Score 1791.8; DB 6; Length 3522;
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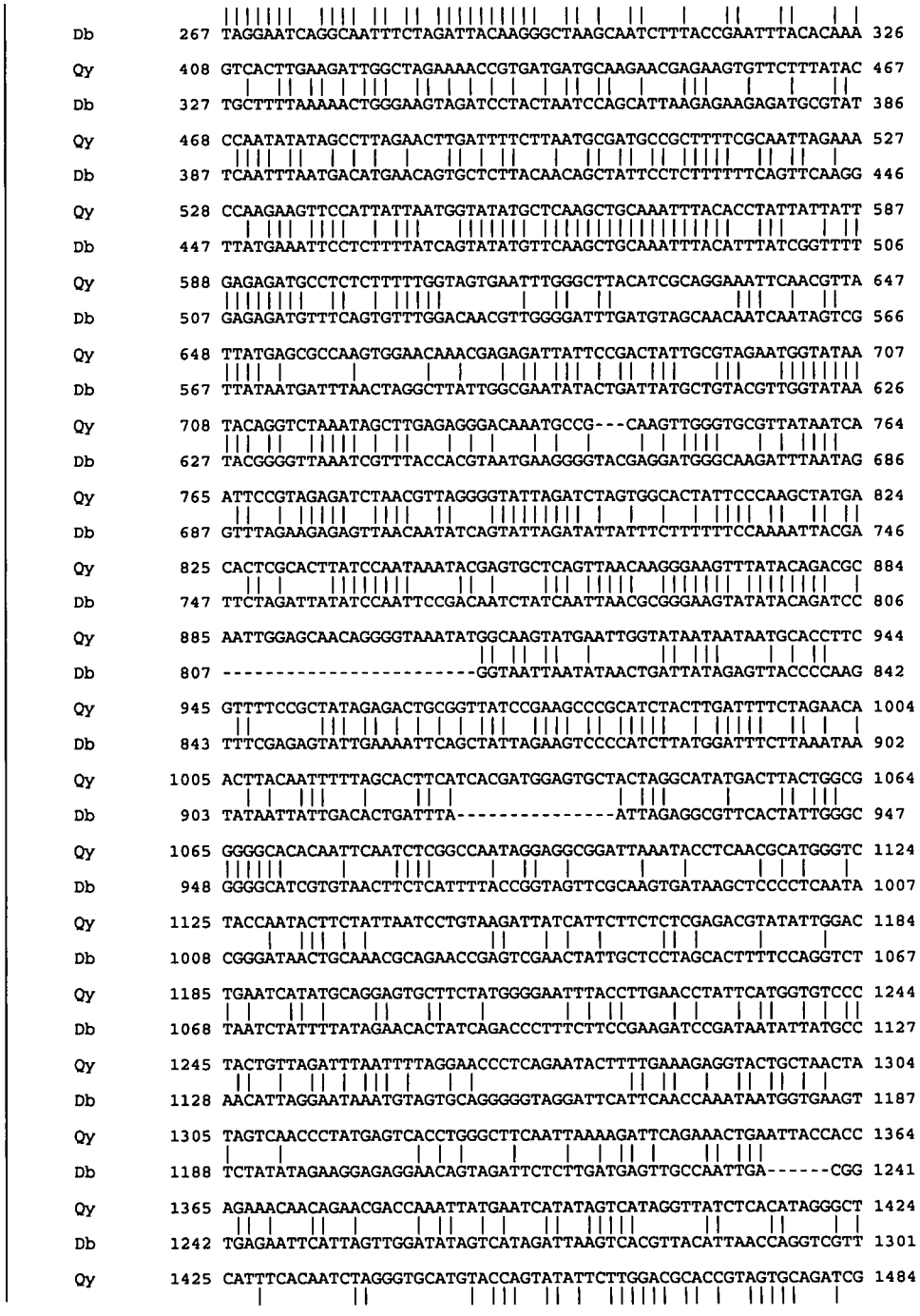

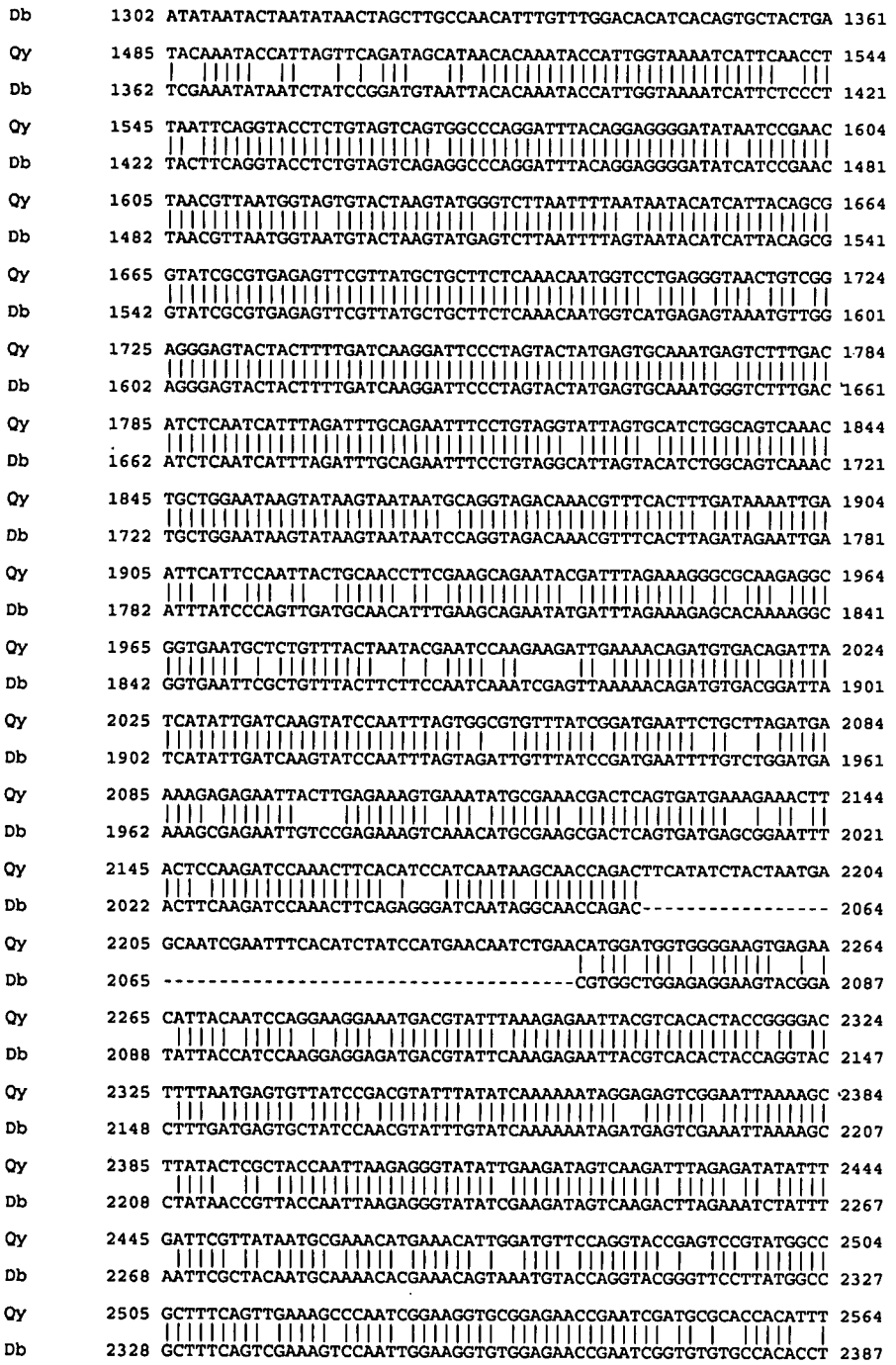
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3	3260.2	88.4	3684	17	US-10-428-961-62	Sequence 62, Appl
4	3133.6	85.0	3687	18	US-10-809-953-9	Sequence 9, Appli
5	1581.6	42.9	3558	9	US-09-826-660-22	Sequence 22, Appl
6	1495.6	40.6	3624	10	US-09-988-462-6	Sequence 6, Appli
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ALIGNMENTS

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; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28
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Query Match 100.0%; Score 3687; DB 17; Length 3687;
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Matches 3687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TTGACTTCAAATAGGAAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAGCTGTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTGACTTCAAATAGGAAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAGCTGTA 60

Qy         61 TCGAATCATTCCACACAAATGGATCTATCACCAGATGCTCGTATTGAGGATTCTTTGTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCGAATCATTCCACACAAATGGATCTATCACCAGATGCTCGTATTGAGGATTCTTTGTGT 120

Qy        121 ATAGCCGAGGGGAATAATATCAATCCACTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATAGCCGAGGGGAATAATATCAATCCACTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180

Qy        181 AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGT 240
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Db        181 AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGT 240

Qy        241 TTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTC 300

Qy        301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
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Db        361 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420

Qy        421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGCC 480
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Db        421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGCC 480

Qy        481 TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA 540
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Db        481 TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA 540

Qy        541 TTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATTGAGAGATGCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATTGAGAGATGCCTCT 600

Qy        601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTATTATGAGCGCCAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTATTATGAGCGCCAA 660

Qy        661 GTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT 720

Qy        721 AGCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCAATTCCGTAGAGATCTA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCAATTCCGTAGAGATCTA 780

Qy        781 ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840
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Db        781 ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840

Qy        841 ATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGCAATTGGAGCAACAGGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGCAATTGGAGCAACAGGG 900

Qy        901 GTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTTTCCGCTATAGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTTTCCGCTATAGAG 960

Qy        961 ACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACAACTTACAATTTTTAGC 1020
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Db        961 ACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACAACTTACAATTTTTAGC 1020

Qy       1021 ACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGGCGGGGGCACACAATTCAA 1080
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Db       1021 ACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGGCGGGGGCACACAATTCAA 1080

Qy       1081 TCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGTCTACCAATACTTCTATT 1140
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Db       1081 TCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGTCTACCAATACTTCTATT 1140

Qy       1141 AATCCTGTAAGATTATCATTCTTCTCTCGAGACGTATATTGGACTGAATCATATGCAGGA 1200
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Db       1141 AATCCTGTAAGATTATCATTCTTCTCTCGAGACGTATATTGGACTGAATCATATGCAGGA 1200

Qy       1201 GTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCCTACTGTTAGATTTAAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCCTACTGTTAGATTTAAT 1260

Qy       1261 TTTAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGTCAACCCTATGAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TTTAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGTCAACCCTATGAG 1320

Qy       1321 TCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACCAGAAACAACAGAACGA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACCAGAAACAACAGAACGA 1380

Qy       1381 CCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCTCATTTCACAATCTAGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCTCATTTCACAATCTAGG 1440

Qy       1441 GTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGATCGTACAAATACCATTAGT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGATCGTACAAATACCATTAGT 1500

Qy       1501 TCAGATAGCATAACACAAATACCATTGGTAAAATCATTCAACCTTAATTCAGGTACCTCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TCAGATAGCATAACACAAATACCATTGGTAAAATCATTCAACCTTAATTCAGGTACCTCT 1560

Qy       1561 GTAGTCAGTGGCCCAGGATTTACAGGAGGGGATATAATCCGAACTAACGTTAATGGTAGT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1621 GTACTAAGTATGGGTCTTAATTTTAATAATACATCATTACAGCGGTATCGCGTGAGAGTT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTACTAAGTATGGGTCTTAATTTTAATAATACATCATTACAGCGGTATCGCGTGAGAGTT 1680

Qy       1681 CGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGTCGGAGGGAGTACTACTTTT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGTCGGAGGGAGTACTACTTTT 1740

Qy       1741 GATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAATCATTTAGA 1800
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Db       1741 GATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAATCATTTAGA 1800

Qy       1801 TTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATA 1860

Qy       1861 AGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATTGAATTCATTCCAATTACT 1920
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Db       1861 AGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATTGAATTCATTCCAATTACT 1920

Qy       1921 GCAACCTTCGAAGCAGAATACGATTTAGAAAGGGCGCAAGAGGCGGTGAATGCTCTGTTT 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GCAACCTTCGAAGCAGAATACGATTTAGAAAGGGCGCAAGAGGCGGTGAATGCTCTGTTT 1980

Qy       1981 ACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATTGATCAAGTA 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 ACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATTGATCAAGTA 2040

Qy       2041 TCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAAGAGAGAATTACTT 2100
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Db       2041 TCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAAGAGAGAATTACTT 2100

Qy       2101 GAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAACTTACTCCAAGATCCAAAC 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAACTTACTCCAAGATCCAAAC 2160

Qy       2161 TTCACATCCATCAATAAGCAACCAGACTTCATATCTACTAATGAGCAATCGAATTTCACA 2220
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Db       2161 TTCACATCCATCAATAAGCAACCAGACTTCATATCTACTAATGAGCAATCGAATTTCACA 2220
Qy       2221 TCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTACAATCCAGGAA 2280
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTACAATCCAGGAA 2280

Qy       2281 GGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGACTTTTAATGAGTGTTAT 2340
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGACTTTTAATGAGTGTTAT 2340

Qy       2341 CCGACGTATTTATATCAAAAAATAGGAGAGTCGGAATTAAAAGCTTATACTCGCTACCAA 2400
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 CCGACGTATTTATATCAAAAAATAGGAGAGTCGGAATTAAAAGCTTATACTCGCTACCAA 2400

Qy       2401 TTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAATGCG 2460
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Db       2401 TTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAATGCG 2460

Qy       2461 AAACATGAAACATTGGATGTTCCAGGTACCGAGTCCGTATGGCCGCTTTCAGTTGAAAGC 2520
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Db       2461 AAACATGAAACATTGGATGTTCCAGGTACCGAGTCCGTATGGCCGCTTTCAGTTGAAAGC 2520

Qy       2521 CCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTTTGAATGGAATCCTGAT 2580
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTTTGAATGGAATCCTGAT 2580

Qy       2581 CTAGATTGTTCCTGCAGAGATGGAGAAAAATGTGCGCATCATTCCCATCATTTCTCTTTG 2640
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 CTAGATTGTTCCTGCAGAGATGGAGAAAAATGTGCGCATCATTCCCATCATTTCTCTTTG 2640

Qy       2641 GATATTGATATTGGATGCACAGACTTGCATGAGAATCTAGGCGTGTGGGTGGTATTCAAG 2700
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Db       2641 GATATTGATATTGGATGCACAGACTTGCATGAGAATCTAGGCGTGTGGGTGGTATTCAAG 2700

Qy       2701 ATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAATCTGGAATTTATTGAAGAGAAACCA 2760
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Db       2701 ATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAATCTGGAATTTATTGAAGAGAAACCA 2760

Qy       2761 TTATTAGGAGAAGCACTGTCTCGTGTGAAGAGAGCAGAGAAAAAATGGAGAGACAAACGT 2820
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Db       2761 TTATTAGGAGAAGCACTGTCTCGTGTGAAGAGAGCAGAGAAAAAATGGAGAGACAAACGT 2820

Qy       2821 GAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAGAAGCTGTGGATGCT 2880
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2881 TTATTTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTGGCATGATTCAT 2940
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Qy       3001 CCGGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCGCATTATCACTGCAATCTCC 3060
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Db       3001 CCGGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCGCATTATCACTGCAATCTCC 3060

Qy       3061 CTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTAGCATGCTGG 3120
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             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 AATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCCTTGTTATCCCA 3180

Qy       3181 GAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGCTATATCCTC 3240
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Db       3181 GAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGCTATATCCTC 3240

Qy       3241 CGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGTTGTGTAACGATCCATGAAATCGAG 3300
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Db       3241 CGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGTTGTGTAACGATCCATGAAATCGAG 3300

Qy       3301 AACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTATCCAACGGAT 3360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3361 ACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGTATGTAATTCCCGTAAT 3420
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Qy       3421 GCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTACAAACCGACT 3480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTACAAACCGACT 3480

Qy       3481 TATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGTGAATATGACAGAGGG 3540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 TATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGTGAATATGACAGAGGG 3540

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Db       3601 GAAACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGGGAAGTTTATTGTAGACAGC 3660

Qy       3661 GTGGAATTACTCCTTATGGAGGAATAG 3687
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Db       3661 GTGGAATTACTCCTTATGGAGGAATAG 3687
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RESULT 2
US-10-428-961-37
; Sequence 37, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 4173
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3687)
US-10-428-961-37

Query Match 99.4%; Score 3666.2; DB 17; Length 4173;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3674; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy          1 TTGACTTCAAATAGGAAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAGCTGTA 60
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Db         61 TCGAATCATTCCACACAAATGGATCTATCACCAGATGCTCGTATTGAGGATTCTTTGTGT 120

Qy        121 ATAGCCGAGGGGAATAATATCAATCCACTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
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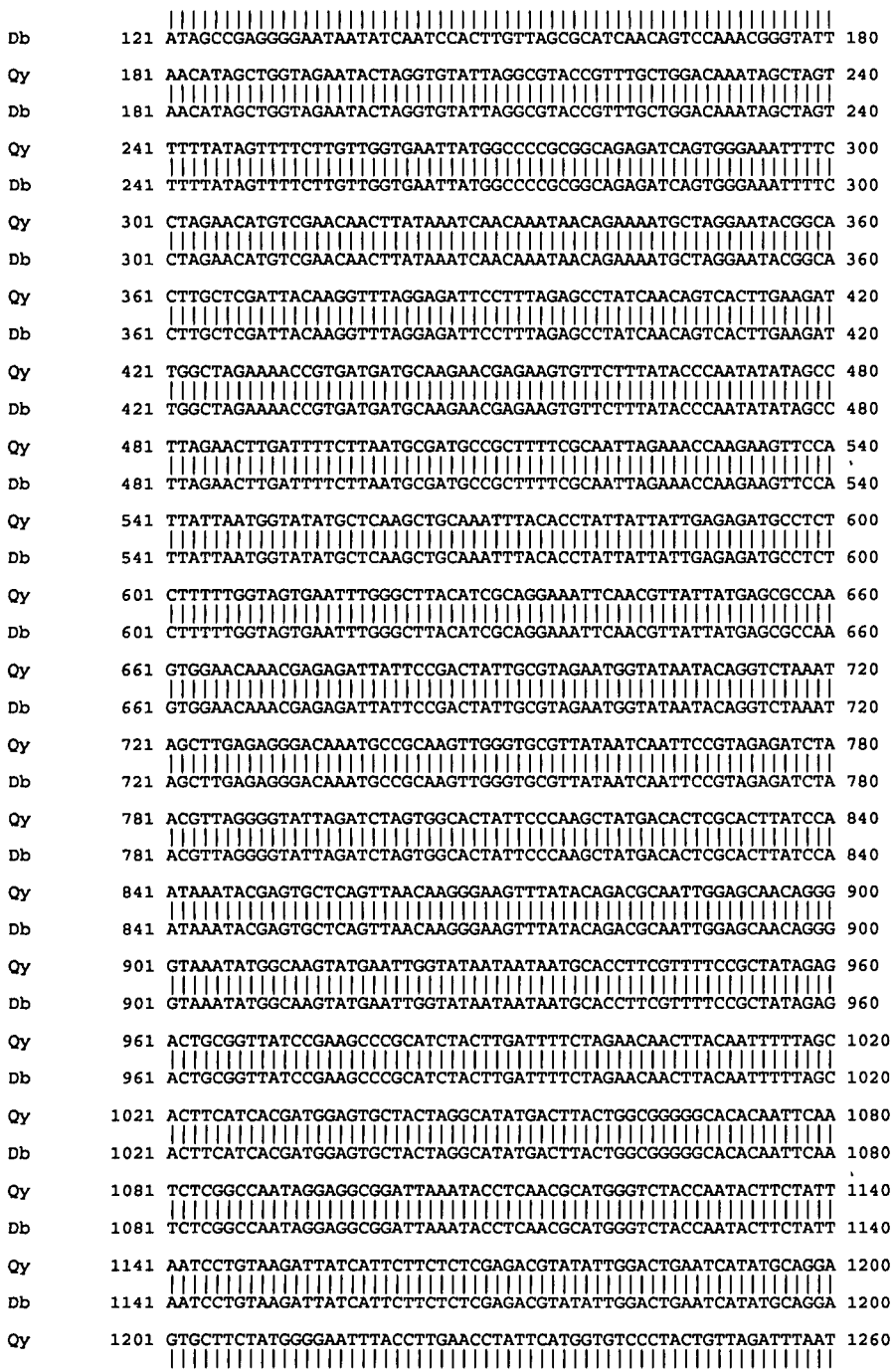
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Qy 241 TTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTC 300
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Qy 301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCA 360
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Qy 481 TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA 540
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Qy 541 TTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATTGAGAGATGCCTCT 600
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Qy 661 GTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT 720
Db 661 GTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT 720
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Db 721 AGCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCAATTCCGTAGAGATCTA 780
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Qy 841 ATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGCAATTGGAGCAACAGGG 900
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Db 901 GTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTTTCCGCTATAGAG 960
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Qy 1021 ACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGGCGGGGGCACACAATTCAA 1080
Db 1021 ACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGGCGGGGGCACACAATTCAA 1080
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Db 1141 AATCCTGTAAGATTATCATTCTTCTCTCGAGACGTATATTGGACTGAATCATATGCAGGA 1200
Qy 1201 GTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCCTACTGTTAGATTTAAT 1260
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Db 1801 TTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATA 1860
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Db 1981 ACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATTGATCAAGTA 2040
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Qy 2221 TCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTACAATCCAGGAA 2280
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Qy 2281 GGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGACTTTTAATGAGTGTTAT 2340
Db 2281 GGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGACTTTTAATGAGTGTTAT 2340

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Qy       2341 CCGACGTATTTATATCAAAAAATAGGAGAGTCGGAATTAAAAGCTTATACTCGCTACCAA 2400
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Db       2341 CCGACGTATTTATATCAAAAAATAGGAGAGTCGGAATTAAAAGCTTATACTCGCTACCAA 2400

Qy       2401 TTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAATGCG 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 TTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAATGCG 2460

Qy       2461 AAACATGAAACATTGGATGTTCCAGGTACCGAGTCCGTATGGCCGCTTTCAGTTGAAAGC 2520
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Qy       2521 CCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTTTGAATGGAATCCTGAT 2580
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 3
US-10-428-961-62
; Sequence 62, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-428-961-62

Query Match 88.4%; Score 3260.2; DB 17; Length 3684;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 3445; Conservative 0; Mismatches 233; Indels 15; Gaps 3;

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Qy        301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCA 360
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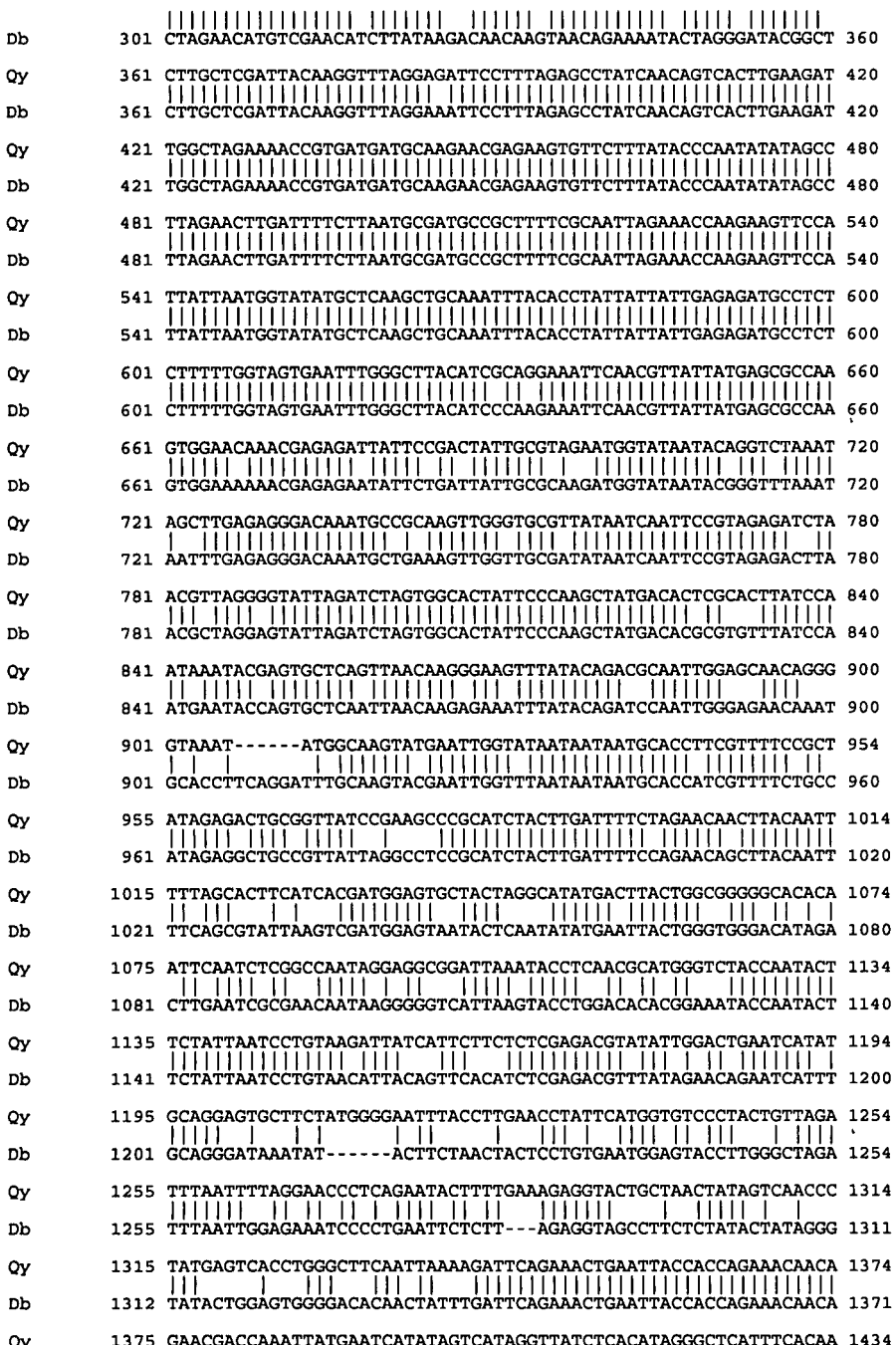
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Db 421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGCC 480
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Db 601 CTTTTTGGTAGTGAATTTGGGCTTACATCCCAAGAAATTCAACGTTATTATGAGCGCCAA 660
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Qy 781 ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840
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Qy 1375 GAACGACCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCTCATTTCACAA 1434
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Qy 1435 TCTAGGGTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGATCGTACAAATACC 1494
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Qy 1555 ACCTCTGTAGTCAGTGGCCCAGGATTTACAGGAGGGGATATAATCCGAACTAACGTTAAT 1614
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Qy 1675 AGAGTTCGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGTCGGAGGGAGTACT 1734
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Qy 1735 ACTTTTGATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAATCA 1794
Db 1732 ACTTTTGATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAATCA 1791
Qy 1795 TTTAGATTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1854
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Qy 2035 CAAGTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAAGAGAGAA 2094
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Db       2692 TTCAAGATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAACCTGGAATTTATTGAAGAG 2751

Qy       2755 AAACCATTATTAGGAGAAGCACTGTCTCGTGTGAAGAGAGCAGAGAAAAAATGGAGAGAC 2814
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Db       2752 AAACCATTATTAGGAGAAGCACTGTCTCGTGTGAAGAGAGCAGAGAAAAAATGGAGAGAC 2811

Qy       2815 AAACGTGAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAGAAGCTGTG 2874
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2812 AAACGTGAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAGAAGCTGTG 2871

Qy       2875 GATGCTTTATTTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTGGCATG 2934
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Db       2872 GATGCTTTATTTGTAGATTCTCAATATGATAGATTACAAGCGGATACAAACATTGGCATG 2931

Qy       2935 ATTCATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCTTATCTGTCAGAATTATCT 2994
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Db       2932 ATTCATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCGTATCTTTCAGAATTATCT 2991

Qy       2995 GTTATCCCGGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCGCATTATCACTGCA 3054
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2992 GTTATCCCAGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCGCATTATCACTGCA 3051

Qy       3055 ATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTAGCA 3114
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3052 ATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTAGCA 3111

Qy       3115 TGCTGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCCTTGTT 3174
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3112 TGCTGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCCTTGTT 3171

Qy       3175 ATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGCTAT 3234
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3172 ATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGCTAT 3231

Qy       3235 ATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGTTGTGTAACGATCCATGAA 3294
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       3232 ATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGTTGTGTAACTATCCATGAA 3291

Qy       3295 ATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTATCCA 3354
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3292 ATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTATCCA 3351

Qy       3355 ACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGTATGTAATTCC 3414
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3352 ACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGTATGTAATTCC 3411

Qy       3415 CGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTACAAA 3474
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3412 CGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTACAAA 3471

Qy       3475 CCGACTTATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGTGAATATGAC 3534
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3472 CCGACTTATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGTGAATATGAC 3531

Qy       3535 AGAGGGTATGTGAATTATCCACCACTACCAGCTGGTTATATGACAAAAGAATTAGAATAC 3594
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       3532 AGAGGGTATGTGAATTATCCACCAGTACCAGCTGGTTATATGACAAAAGAATTAGAATAC 3591

Qy       3595 TTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGGGAAGTTTATTGTA 3654
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3592 TTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGGGAAGTTTATTGTA 3651

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Db       3652 GACAGCGTGGAATTACTCCTTATGGAGGAATAG 3684
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RESULT 4
US-10-809-953-9
; Sequence 9, Application US/10809953
; Publication No. US20040181825A1
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTI
; TITLE OF INVENTION: CRYSTAL PROTEINS
; FILE REFERENCE: 021565-078
; CURRENT APPLICATION NUMBER: US/10/809,953
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/661,016
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/EP90/00905
; PRIOR FILING DATE: 1990-05-30
; PRIOR APPLICATION NUMBER: GB 89401499.2
; PRIOR FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 3687
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3687)
US-10-809-953-9

Query Match 85.0%; Score 3133.6; DB 18; Length 3687;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 3373; Conservative 0; Mismatches 299; Indels 30; Gaps 3;

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Qy         61 TCGAATCATTCCACACAAATGGATCTATCACCAGATGCTCGTATTGAGGATTCTTTGTGT 120
              |||||||||||| |||||||||||||||| |||||||||||||||||||||||||||||||
Db         46 TCGAATCATTCCGCACAAATGGATCTATTACCAGATGCTCGTATTGAGGATAGCTTGTGT 105

Qy        121 ATAGCCGAGGGGAATAATATCAATCCACTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
              |||||||||||||| |||||  ||||| |||||||||||||||||||||||||||||||||
Db        106 ATAGCCGAGGGGAACAATATTGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATT 165

Qy        181 AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGT 240
              |||||||||||||||||||| ||||| |||||||||||||||||| ||||||||||||||
Db        166 AACATAGCTGGTAGAATACTAGGCGTATTGGGCGTACCGTTTGCTGGACAACTAGCTAGT 225

Qy        241 TTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 TTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTC 285

Qy        301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCT 345

Qy        361 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        346 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTCAGAGCCTATCAACAGTCACTTGAAGAT 405

Qy        421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGCC 480
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Db        406 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTCATACCCAATATATAGCT 465

Qy        481 TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA 540
Db        466 TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA 525

Qy        541 TTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATTGAGAGATGCCTCT 600
Db        526 TTATTGATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATTGAGAGATGCCTCT 585

Qy        601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTATTATGAGCGCCAA 660
Db        586 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGCTATTATGAGCGCCAA 645

Qy        661 GTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT 720
Db        646 GTGGAACGAACGAGAGATTATTCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT 705

Qy        721 AGCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCAATTCCGTAGAGATCTA 780
Db        706 AGCTTGAGAGGGACAAATGCCGCAAGTTGGGTACGGTATAATCAATTCCGTAGAGATCTA 765

Qy        781 ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840
Db        766 ACGTTAGGAGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 825

Qy        841 ATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGCAATTGGAGCAACAGGG 900
Db        826 ATAAATACGAGTGCTCAGTTAACAAGAGAAGTTTATACAGACGCAATTGGAGCAACAGGG 885

Qy        901 GTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTTTCCGCTATAGAG 960
Db        886 GTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTCTCTGCCATAGAG 945

Qy        961 ACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACAACTTACAATTTTTAGC 1020
Db        946 GCTGCGGCTATCCGAAGCCCGCATCTACTTGATTTCTAGAACAACTTACAATTTTTAGC 1005

Qy       1021 ACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGGCGGGGGCACACAATTCAA 1080
Db       1006 GCTTCATCACGATGGAGTAATACTAGGCATATGACTTATTGGCGGGGGCACACGATTCAA 1065

Qy       1081 TCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGTCTACCAATACTTCTATT 1140
Db       1066 TCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGGCTACCAATACTTCTATT 1125

Qy       1141 AATCCTGTAAGATTATCATTCTTCTCTCGAGACGTATATTGGACTGAATCATATGCAGGA 1200
Db       1126 AATCCTGTAACATTACGGTTCGCATCTCGAGACGTTTATAGGACTGAATCATATGCAGGA 1185

Qy       1201 GTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCCTACTGTTAGATTTAAT 1260
Db       1186 GTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCCTACTGTTAGGTTTAAT 1245

Qy       1261 TTTAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGTCAACCCTATGAG 1320
Db       1246 TTTACGAACCCTCAGAATATTTCTGATAGAGGTACCGCTAACTATAGTCAACCTTATGAG 1305

Qy       1321 TCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACCAGAAACAACAGAACGA 1380
Db       1306 TCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACCAGAAACAACAGAACGA 1365

Qy       1381 CCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCTCATTTCACAATCTAGG 1440
Db       1366 CCAAATTATGAATCTTACAGTCACAGGTTATCTCATATAGGTATAATTTTACAATCCAGG 1425

Qy       1441 GTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGATCGTACAAATACCATTAGT 1500
Db       1426 GTGAATGTACCGGTATATTCTTGGACGCATCGTAGTGCAGATCGTACGAATACGATTGGA 1485

Qy       1501 TCAGATAGCATAACACAAATACCATTGGTAAAATCATTCAACCTTAATTCAGGTACCTCT 1560

Db       1486 CCAAATAGAATCACCCAAATCCCAATGGTAAAAGCATCCGAACTTCCTCAAGGTACCACT 1545

Qy       1561 GTAGTCAGTGGCCCAGGATTTACAGGAGGGGATATAATCCGAACTAACGTTAATGGTAGT 1620
Db       1546 GTTGTTAGAGGACCAGGATTTACTGGTGGGGATATTCTTCGAAGAACGAATACTGGTGGA 1605

Qy       1621 GTACTAAGTATGGGTCTTAATTTTAATAATACATCATTACAGCGGTATCGCGTGAGAGTT 1680
Db       1606 TTTGGACCGATAAGAGTAACTGTTAACGGACCATTAACACAAAGATATCGTATAGGATTC 1665

Qy       1681 CGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGTCGGAGGGAGTACTACTTTT 1740
Db       1666 CGCTATGCTTCAACTGTAGATTTTGATTTCTTTGTATCACGTGGAGGTACTACTGTAAAT 1725

Qy       1741 GATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAATCATTTAGA 1800
Db       1726 AATTTTAGATTCCTACGTACAATGAACAGTGGAGACGAACTAAAATACGGAAATTTTGTG 1785

Qy       1801 TTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAA---ACTGCTGGAATAAGT 1857
Db       1786 AGACGTGCTTTTACTACACCTTTTACTTTTACACAAATTCAAGATATAATTCGAACGTCT 1845

Qy       1858 ATAAGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATTGAATTCATTCCAATT 1917
Db       1846 ATTCAAGGCCTTAGTGGAAATGGGGAAGTGTATATAGATAAAATTGAAATTATTCCAGTT 1905

Qy       1918 ACTGCAACCTTCGAAGCAGAATACGATTTAGAAAGGGCGCAAGAGGCGGTGAATGCTCTG 1977
Db       1906 ACTGCAACCTTCGAAGCAGAATATGATTTAGAAAGAGCGCAAGAGGCGGTGAATGCTCTG 1965

Qy       1978 TTTACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATTGATCAA 2037
Db       1966 TTTACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATTGATCAA 2025

Qy       2038 GTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAAGAGAGAATTA 2097
Db       2026 GTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTGGATGAAAAGAGAGAATTA 2085

Qy       2098 CTTGAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAACTTACTCCAAGATCCA 2157
Db       2086 CTTGAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAACTTACTCCAAGATCCA 2145

Qy       2158 AACTTCACATCCATCAATAAGCAACCAGACTTCATATCTACTAATGAGCAATCGAATTTC 2217
Db       2146 AACTTCACATCCATCAATAAGCAACCAGACTTCATATCTACTAATGAGCAATCGAATTTC 2205

Qy       2218 ACATCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTACAATCCAG 2277
Db       2206 ACATCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTACCATCCAG 2265

Qy       2278 GAAGGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGACTTTTAATGAGTGT 2337
Db       2266 GAAGGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGTACTTTTAATGAGTGT 2325

Qy       2338 TATCCGACGTATTTATATCAAAAAATAGGAGAGTCGGAATTAAAAGCTTATACTCGCTAC 2397
Db       2326 TATCCGACGTATTTATATCAAAAAATAGGGGAGTCGGAATTAAAAGCTTATACTCGCTAC 2385

Qy       2398 CAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAAT 2457
Db       2386 CAATTAAGAGGTTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAAT 2445

Qy       2458 GCGAAACATGAAACATTGGATGTTCCAGGTACCGAGTCCGTATGGCCGCTTTCAGTTGAA 2517
Db       2446 GCGAAACATGAAACATTGGATGTTCCAGGTACCGAGTCCCTATGGCCGCTTTCAGTTGAA 2505

Qy       2518 AGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTTTGAATGGAATCCT 2577
Db       2506 AGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTTTGAATGGAATCCT 2565

Qy       2578 GATCTAGATTGTTCCTGCAGAGATGGAGAAAAATGTGCGCATCATTCCCATCATTTCTCT 2637
Db       2566 GATCTAGATTGTTCCTGCAGAGATGGAGAAAAATGTGCGCATCATTCCCATCATTTCTCT 2625
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Qy       2638 TTGGATATTGATATTGGATGCACAGACTTGCATGAGAATCTAGGCGTGTGGGTGGTATTC 2697
Db       2626 TTGGATATTGATGTTGGATGCACAGACTTGCATGAGAATCTAGGCGTGTGGGTGGTATTC 2685

Qy       2698 AAGATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAATCTGGAATTTATTGAAGAGAAA 2757
Db       2686 AAGATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAATCTGGAATTTATTGAAGAGAAA 2745

Qy       2758 CCATTATTAGGAGAAGCACTGTCTCGTGTGAAGAGAGCAGAGAAAAAATGGAGAGACAAA 2817
Db       2746 CCATTATTAGGAGAAGCACTGTCTCGTGTGAAGAGGGCAGAGAAAAAATGGAGAGACAAA 2805

Qy       2818 CGTGAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAGAAGCTGTGGAT 2877
Db       2806 CGTGAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAGAAGCTGTGGAT 2865

Qy       2878 GCTTTATTTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTGGCATGATT 2937
Db       2866 GCTTTATTCGTAGATTCTCAATATGATAGATTACAAGCGGATACAAACATCGGCATGATT 2925

Qy       2938 CATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCTTATCTGTCAGAATTATCTGTT 2997
Db       2926 CATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCGTATCTTTCAGAATTACCTGTT 2985

Qy       2998 ATCCCGGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCGCATTATCACTGCAATC 3057
Db       2986 ATCCCAGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCACATTATCACTGCAATC 3045

Qy       3058 TCCCTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTAGCATGC 3117
Db       3046 TCCTTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTAACATGT 3105

Qy       3118 TGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCCTTGTTATC 3177
Db       3106 TGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCATCGTTCTGACCTTGTTATC 3165

Qy       3178 CCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGCTATATC 3237
Db       3166 CCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGTGTGGCTATATC 3225

Qy       3238 CTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGTTGTGTAACGATCCATGAAATC 3297
Db       3226 CTTCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGGCTGCGTAACGATCCATGAAATC 3285

Qy       3298 GAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTATCCAACG 3357
Db       3286 GAGAACAATACAGACGAACTAAAATTTAAAAACCGTGAAGAAGAGGAAGTGTATCCAACG 3345

Qy       3358 GATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGC----------AGTA 3405
Db       3346 GATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCTGGATGCGCAGATGCA 3405

Qy       3406 TGTAATTCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTT 3465
Db       3406 TGTAATTCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTT 3465

Qy       3466 AATTACAAACCGACTTATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGT 3525
Db       3466 AATTACAAACCGACTTATGAAGAAGAAACGTATACAGATGTAAGAAGAGATAATCATTGT 3525

Qy       3526 GAATATGACAGAGGGTATGTGAATTATCCACCACTACCAGCTGGTTATATGACAAAAGAA 3585
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Qy       3586 TTAGAATACTTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGGGAAG 3645
Db       3586 TTAGAATACTTCCCAGAAACAGATACAGTATGGATTGAGATTGGAGAAACGGAAGGAAAG 3645

Qy       3646 TTTATTGTAGACAGCGTGGAATTACTCCTTATGGAGGAATAG 3687
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RESULT 5
US-09-826-660-22
; Sequence 22, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
;  APPLICANT: Cardineau, Guy A.
;  APPLICANT:  Stelman, Steven J.
;  APPLICANT:  Narva, Kenneth E.
;  TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
;  FILE REFERENCE: MA-714XC2D1
;  CURRENT APPLICATION NUMBER: US/09/826,660
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 09/178,252
;  PRIOR FILING DATE: 1998-10-23
;  PRIOR APPLICATION NUMBER: 60/065,215
;  PRIOR FILING DATE: 1997-11-12
;  PRIOR APPLICATION NUMBER: 60/076,445
;  PRIOR FILING DATE: 1998-03-02
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 3558
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-826-660-22

  Query Match           42.9%;  Score 1581.6;  DB 9;  Length 3558;
  Best Local Similarity   66.5%;  Pred. No. 0;
  Matches 2458;  Conservative    0;  Mismatches 1084;  Indels  156;  Gaps    7;

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Qy         62 CGAATCATTCCACACAAATGGATCTATCACCAGATGCTCGTATTGAGGATTCTTTGTGTA 121
Db         62 CTAACCATTCTGCTCAGATGAACCTTTCTACTGATGCTAGAATCGAGGATTCTCTTTGCA 121

Qy        122 TAGCCGAGGGGAATAATATCAATCCACTTGTTAGCGCATCAACAGTCCAAACGGGTATTA 181
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Qy        182 ACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGTT 241
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Qy        242 TTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTCC 301
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Qy        302 TAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCAC 361
Db        302 TTGAGCATGTTGAGCAGTTGATTCGTCAACAAGTTACTGAGAACACTAGAGATACTGCTC 361

Qy        362 TTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGATT 421
Db        362 TTGCTAGACTTCAAGGACTTGGAAACTCTTTCAGAGCTTACCAACAATCTCTTGAGGATT 421

Qy        422 GGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGCCT 481
Db        422 GGCTTGAGAACAGAGATGATGCTAGAACTAGATCTGTGTTGTACACTCAGTACATTGCTC 481

Qy        482 TAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCAT 541
Db        482 TTGAGCTTGACTTCTTGAACGCTATGCCATTGTTCGCTATCAGAAACCAAGAGGTTCCAC 541

Qy        542 TATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATTGAGAGATGCCTCTC 601
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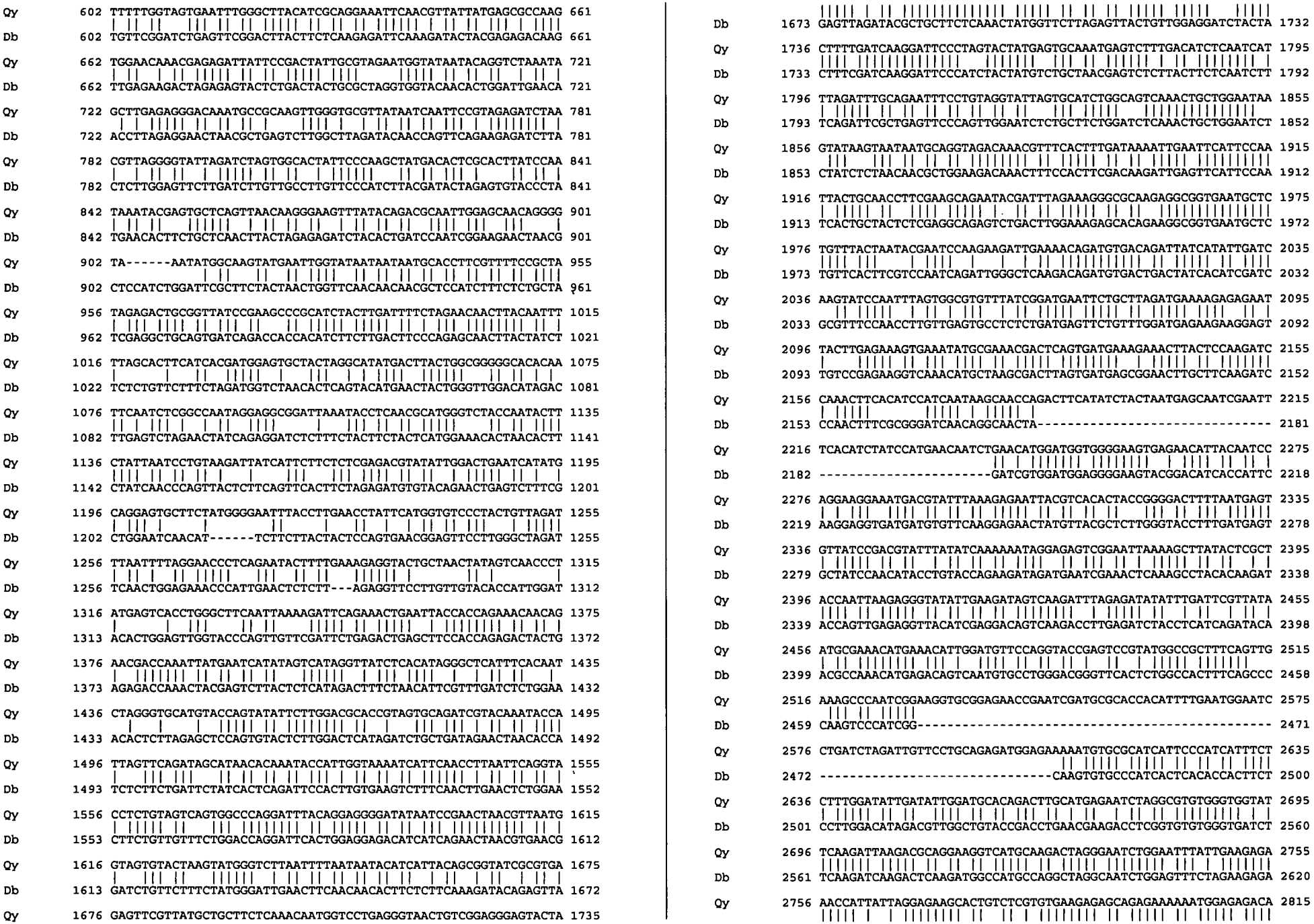

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Db       2621 AACCACTTGTTGGAGAAGCCCTCGCTAGAGTGAAGAGGGCTGAGAAGAAGTGGAGGGACA 2680

Qy       2816 AACGTGAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAGAAGCTGTGG 2875

Db       2681 AGAGAGAGAAGTTGGAATGGGAAACAAACATTGTGTACAAAGAAGCCAAAGAAAGCGTTG 2740

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Db       3521 TCATTGTTGATAGCGTGGAGTTACTTCTGATGGAGGAA 3558


RESULT 6
US-09-988-462-6
; Sequence 6, Application US/09988462
; Publication No. US20030046726A1
;  GENERAL INFORMATION:
;       APPLICANT: Koziel, Michael G.
;                  Desai, Nalini M.
;                  Lewis, Kelly S.
;                  Kramer, Vance C.
;                  Warren, Gregory W.
;                  Evola, Stephen V.
;                  Crossland, Lyle D.
;                  Wright, Martha S.
;                  Merlin, Ellis J.
;                  Launis, Karen L.
;       TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;                           INSECTICIDAL ACTIVITY IN MAIZE
;       NUMBER OF SEQUENCES: 94
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Syngenta Biotechnology, Inc.
;            STREET: 3054 Cornwallis Road
;            CITY: Research Triangle Park
;            STATE: NC
;            COUNTRY: USA
;            ZIP: 27709
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/988,462
;            FILING DATE: 20-No. US20030046726A1-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 09/547,422
;            FILING DATE: 11-APR-2000
;            APPLICATION NUMBER: US 08/459,504
;            FILING DATE: 02-JUN-1995
;            APPLICATION NUMBER: US 07/951,715
;            FILING DATE: 25-SEP-1992
;            APPLICATION NUMBER: US 07/772,027
;            FILING DATE: 04-OCT-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Meigs, J. Timothy
;            REGISTRATION NUMBER: 38,241
;            REFERENCE/DOCKET NUMBER: S-18805I
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (919)541-8587
;            TELEFAX: (919)541-8689
;  INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 3624 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "Synthetic DNA"
;       HYPOTHETICAL: NO
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  1..3621
;            OTHER INFORMATION:  /product= "Full-length, maize
;            optmized cryIB"
;            /note= "Disclosed in Figure 6."
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-988-462-6

  Query Match             40.6%;  Score 1495.6;  DB 10;  Length 3624;
  Best Local Similarity   63.7%;  Pred. No. 0;
  Matches 2310;  Conservative    0;  Mismatches 1299;  Indels   15;  Gaps    2;

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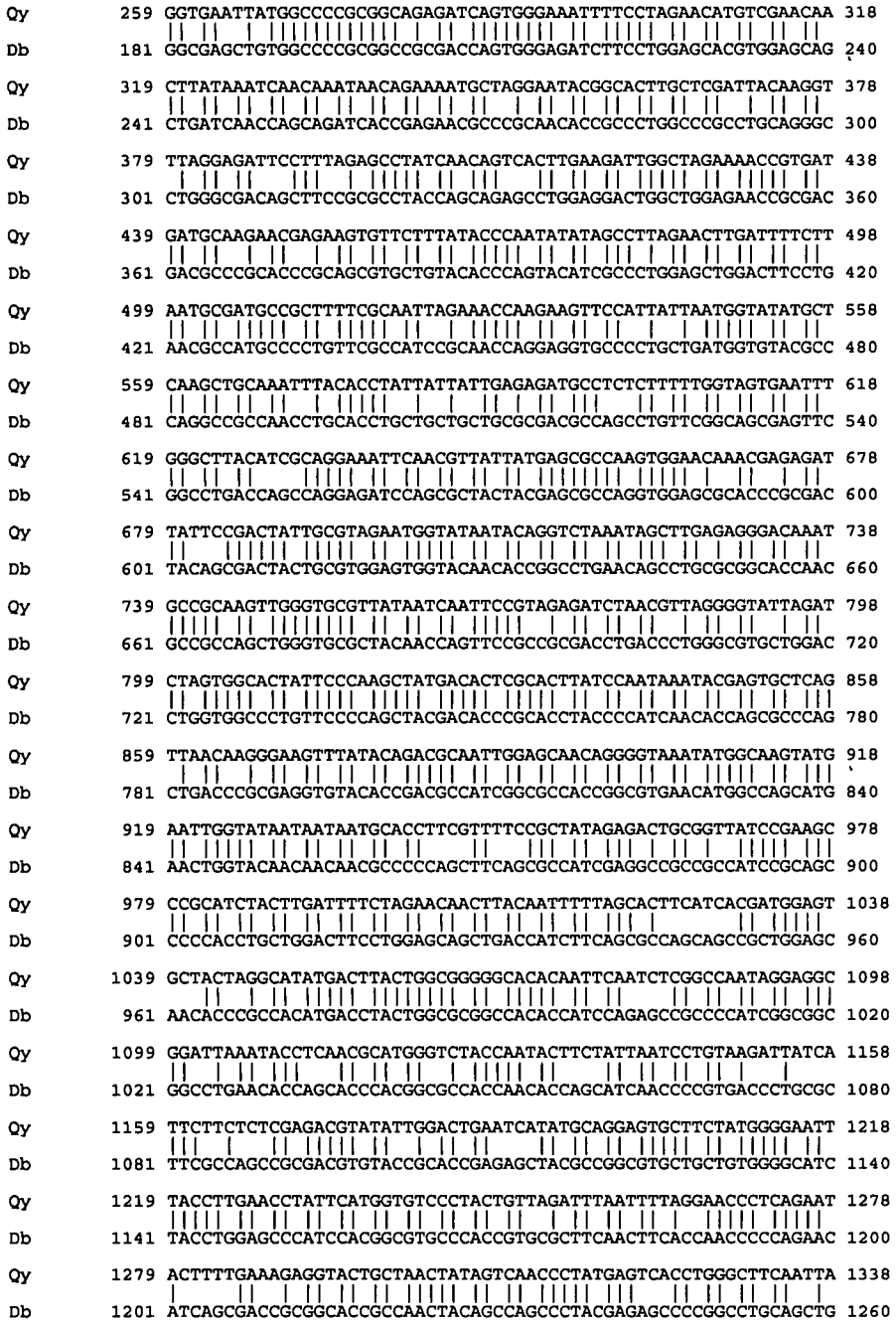

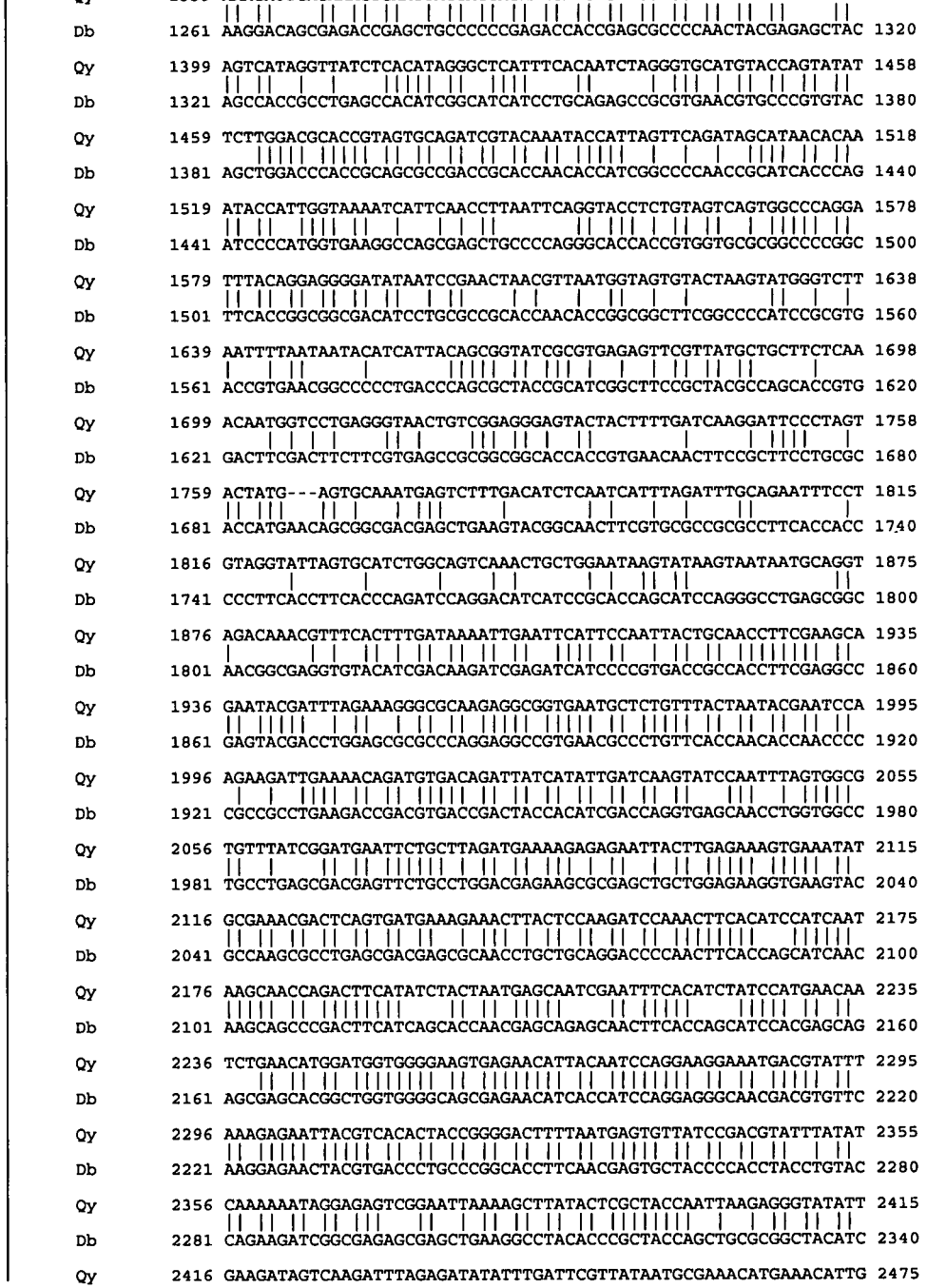

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Qy       2716 GGTCATGCAAGACTAGGGAATCTGGAATTTATTGAAGAGAAACCATTATTAGGAGAAGCA 2775
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Db       2701 CTGAGCCGCGTGAAGCGCGCCGAGAAGAAGTGGCGCGACAAGCGCGAGAAGCTGCAGCTG 2760
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Qy       2896 CAATATAATAGATTACAAGCGGATACAAACATTGGCATGATTCATGCGGCAGATAAACTT 2955
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Qy       2956 GTTCATCGAATTCGAGAGGCTTATCTGTCAGAATTATCTGTTATCCCGGGTGTAAATGCG 3015
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Qy       3016 GAAATTTTTGAAGAATTAGAAGGTCGCATTATCACTGCAATCTCCCTATACGATGCGAGA 3075
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Qy       3076 AATGTCGTTAAAAATGGTGATTTTAATAATGGATTAGCATGCTGGAATGTAAAAGGGCAT 3135
Db       3001 AACGTGGTGAAGAACGGCGACTTCAACAACGGCCTGACCTGCTGGAACGTGAAGGGCCAC 3060
Qy       3136 GTAGATGTACAACAGAGCCATCACCGTTCTGTCCTTGTTATCCCAGAATGGGAAGCAGAA 3195
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Qy       3256 AAAGAGGGATATGGAGAGGGTTGTGTAACGATCCATGAAATCGAGAACAATACAGACGAA 3315
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Qy       3316 CTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTATCCAACGGATACAGGAACGTGTAAT 3375
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Qy       3376 GATTATACTGCACACCAAGGTACAGC----------AGTATGTAATTCCCGTAATGCT 3423
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Qy       3424 GGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTACAAACCGACTTAT 3483
Db       3361 GGCTACGAGGACGCCTACGAGGTGGACACCACCGCCAGCGTGAACTACAAGCCCACCTAC 3420
Qy       3484 GAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGTGAATATGACAGAGGGTAT 3543
Db       3421 GAGGAGGAGACCTACACCGACGTGCGCCGCGACAACCACTGCGAGTACGACCGCGGCTAC 3480
Qy       3544 GTGAATTATCCACCACTACCAGCTGGTTATATGACAAAAGAATTAGAATACTTCCCAGAA 3603
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Qy       3604 ACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGGGAAGTTTATTGTAGACAGCGTG 3663
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RESULT 7
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; Sequence 5, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 3522
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-826-660-5

Query Match 38.2%; Score 1408.4; DB 9; Length 3522;
Best Local Similarity 65.7%; Pred. No. 0;
Matches 2243; Conservative 0; Mismatches 1061; Indels 108; Gaps 9;

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Qy        345 TGCTAGGAATACGGCACTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCA 404
Db        267 GGAAAGGAACCGGGCAATTACTACATTACGAGGGTTAGCAGATAGCTATGAAATTTATAT 326
Qy        405 ACAGTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTA 464
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Qy        525 AAACCAAGAAGTTCCATTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATT 584
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Qy        585 ATTGAGAGATGCCCTCTCTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACG 644
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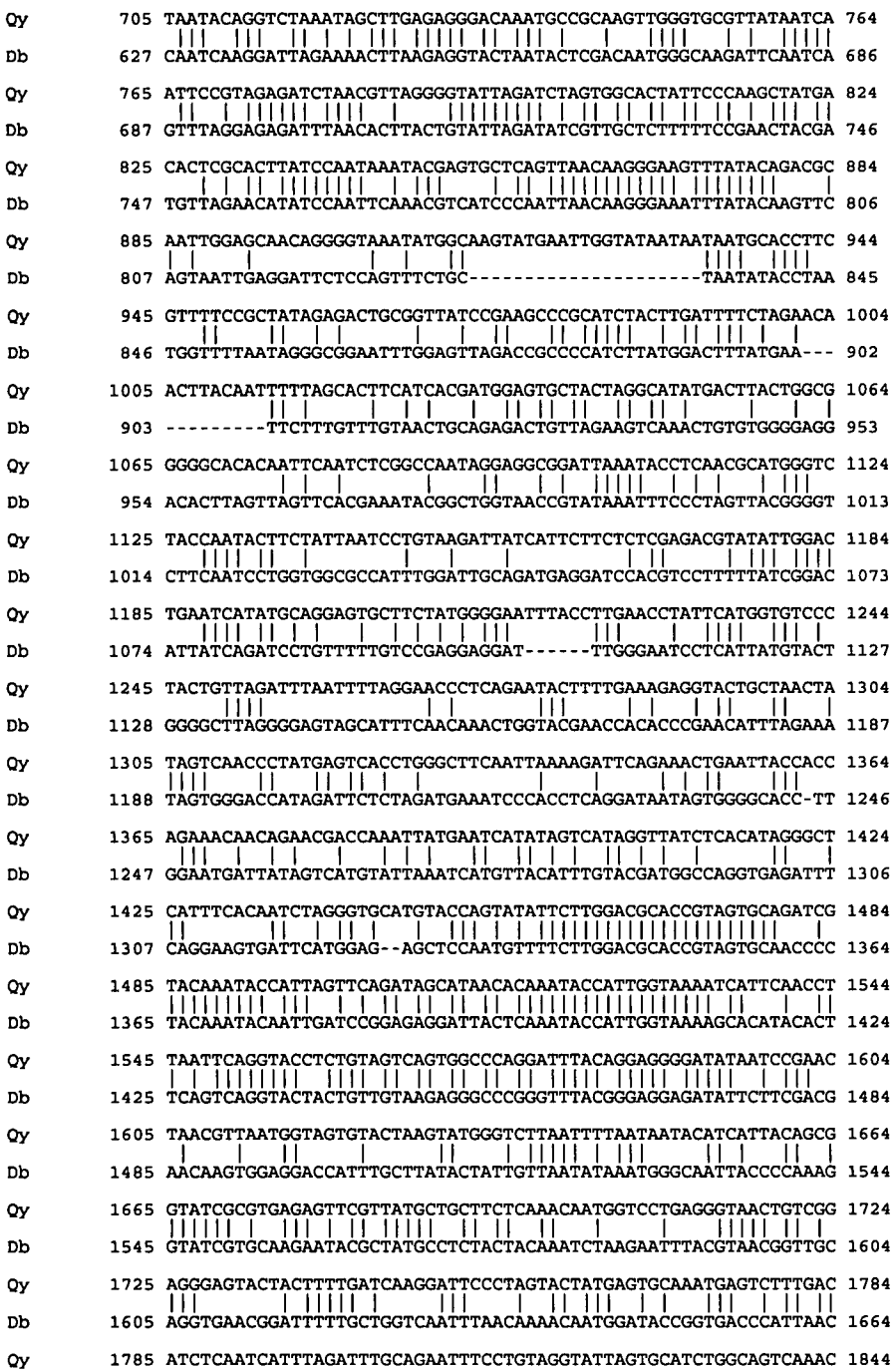

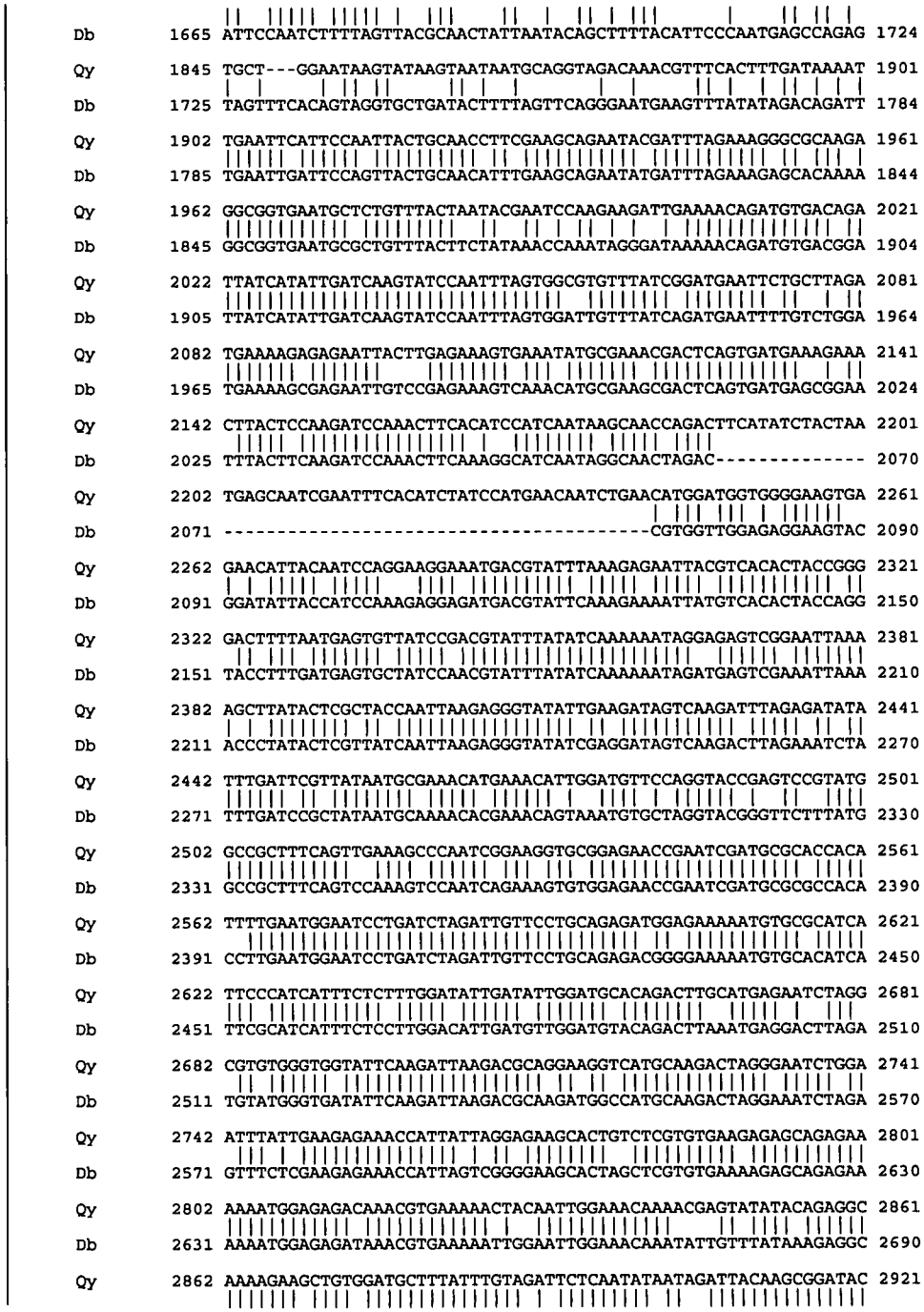

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RESULT 8
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; Sequence 7, Application US/09837961
; Publication No. US20040058860A1
; GENERAL INFORMATION:
;  APPLICANT: Payne, Jewel
;  APPLICANT:  Sick, August
;  TITLE OF INVENTION: No. US20040058860A1el Bacillus thuringiensis Isolate Active Again
;  TITLE OF INVENTION:  and Genes Encoding No. US20040058860A1el Lepidopteran-Active Tox
;  FILE REFERENCE: MA-43CDF2D3
;  CURRENT APPLICATION NUMBER: US/09/837,961
;  CURRENT FILING DATE:  2001-04-19
;  PRIOR APPLICATION NUMBER: US 09/521,344
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: US 08/933,891
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: US 08/356,034
;  PRIOR FILING DATE: 1994-12-14
;  PRIOR APPLICATION NUMBER: US 08/210,110
;  PRIOR FILING DATE: 1994-03-17
;  PRIOR APPLICATION NUMBER: US 07/865,168
;  PRIOR FILING DATE: 1992-04-09
;  PRIOR APPLICATION NUMBER: US 07/451,261
;  PRIOR FILING DATE: 1989-12-14
;  PRIOR APPLICATION NUMBER: US 371,955
;  PRIOR FILING DATE: 1989-06-27
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;  LENGTH: 3522
;  TYPE: DNA
;  ORGANISM: Bacillus thuringiensis
US-09-837-961-7

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  Matches 2243;  Conservative    0;  Mismatches 1061;  Indels  108;  Gaps    9;

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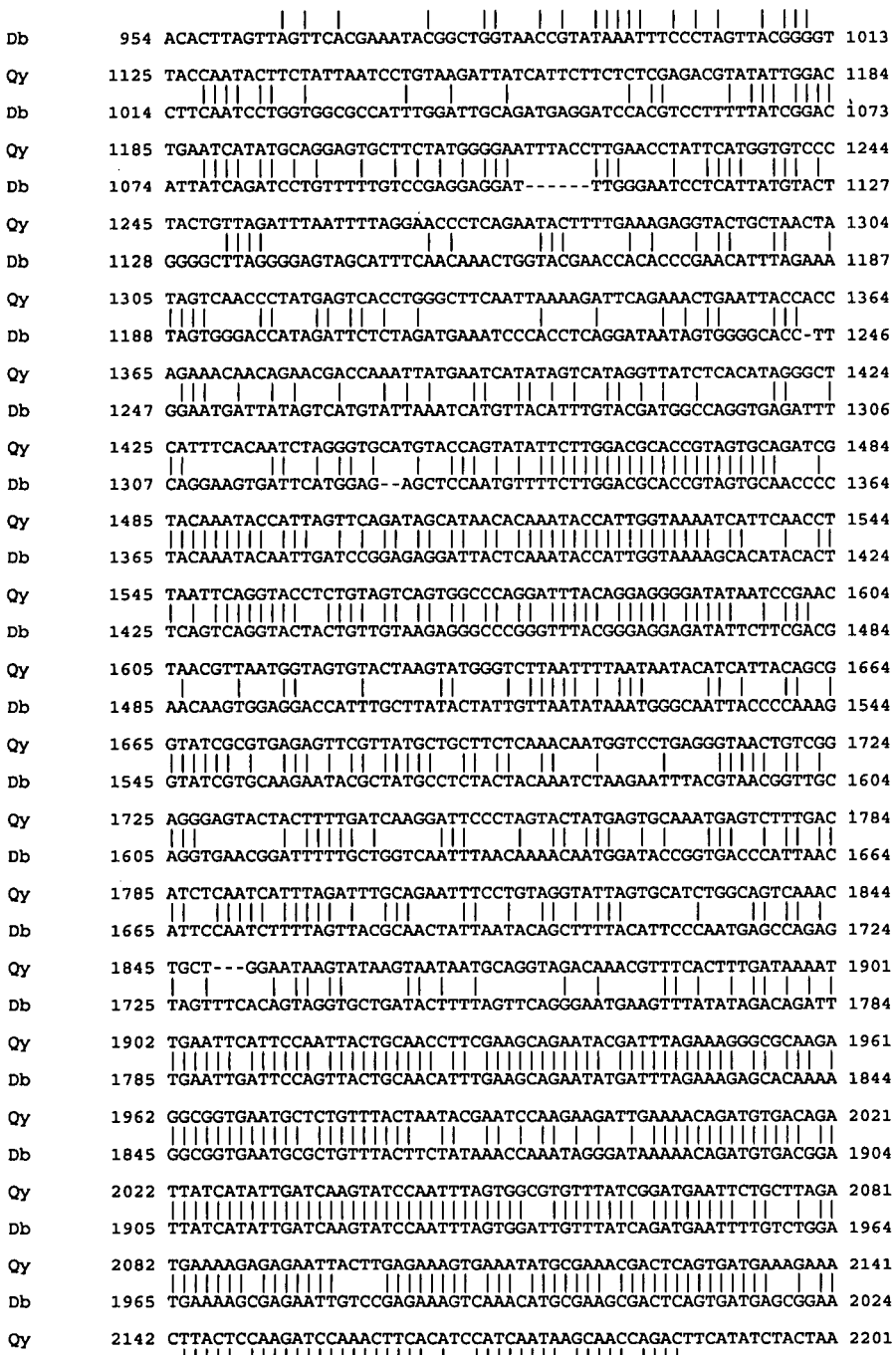

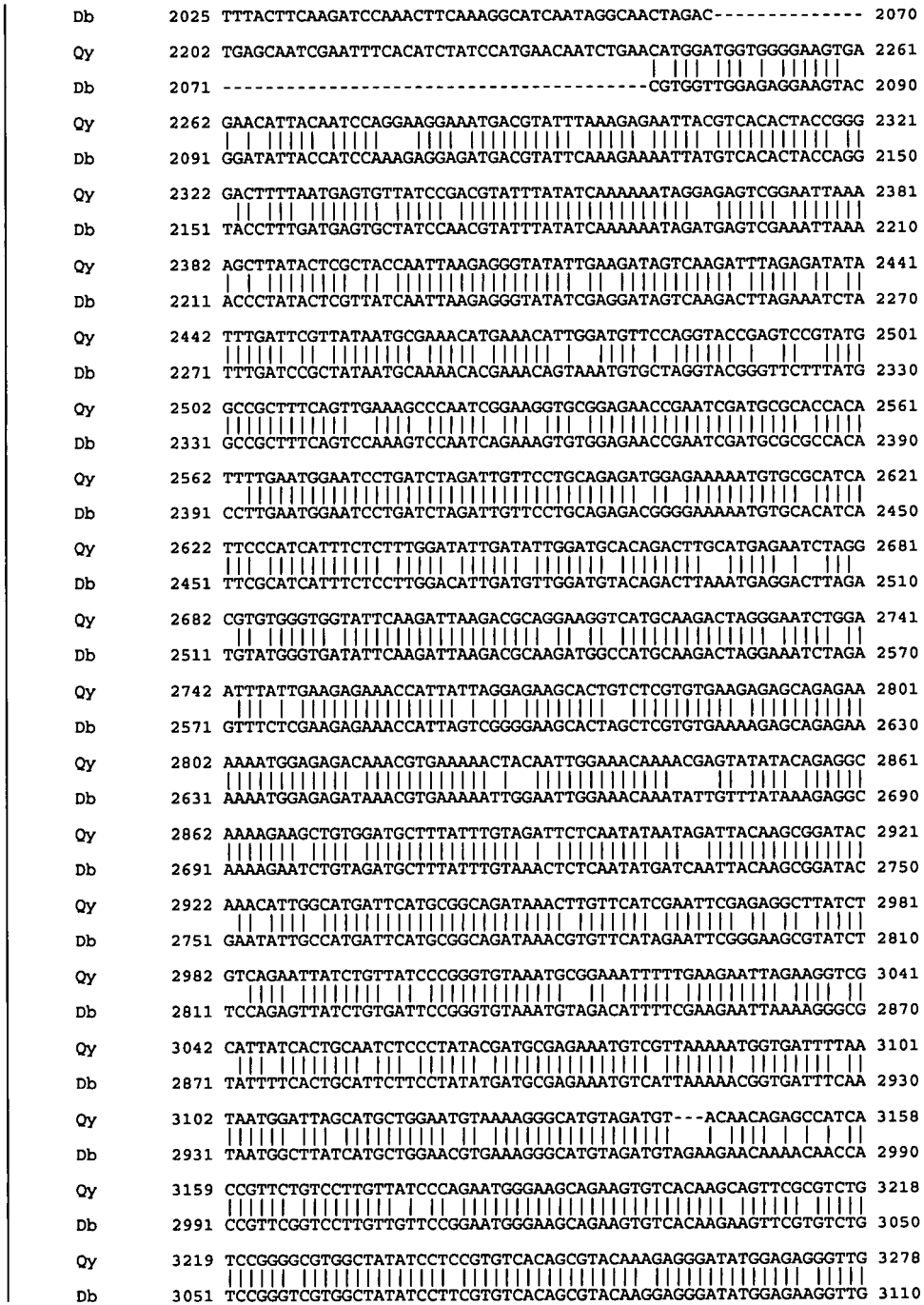

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Db       3231 ATACGGGGGTGCGTACACTTCCCGTAATCGTGGATATGACGAAACTTATGGAAGCAATTC 3290

Qy       3453 TACAGCATCTGTTAATTACAAACCGACTTATGAAGAAGAAACGTATACAGATGTACGAAG 3512
Db       3291 TTCTGTACCAGCTGATTATGCGTCAGTCTATGAAGAAAAATCGTATACAGATGGACGAAG 3350

Qy       3513 AGATAATCATTGTGAATATGACAGAGGGTATGTGAATTATCCACCACTACCAGCTGGTTA 3572
Db       3351 AGACAATCCTTGTGAATCTAACAGAGGATATGGGGATTACACACCACTACCAGCTGGCTA 3410

Qy       3573 TATGACAAAAGAATTAGAATACTTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGA 3632
Db       3411 TGTGACAAAAGAATTAGAGTACTTCCCAGAAACCGATAAGGTATGGATTGAGATCGGAGA 3470

Qy       3633 AACGGAAGGGAAGTTTATTGTAGACAGCGTGGAATTACTCCTTATGGAGGAA 3684
Db       3471 AACGGAAGGAACATTCATCGTGGACAGCGTGGAATTACTCCTTATGGAGGAA 3522
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RESULT 9
US-10-825-751-7
; Sequence 7, Application US/10825751
; Publication No. US20040194165A1
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: Novel Bacillus thuringiensis Isolate Active Against Lepidopteran
; TITLE OF INVENTION: Pests, and Genes Encoding Novel Lepidopteran-Active Toxins
; FILE REFERENCE: MA-43CDF2D4
; CURRENT APPLICATION NUMBER: US/10/825,751
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 09/837,961
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/521,344
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 08/933,891
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: US 08/356,034
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: US 08/210,110
; PRIOR FILING DATE: 1994-03-17
; PRIOR APPLICATION NUMBER: US 07/865,168
; PRIOR FILING DATE: 1992-04-09
; PRIOR APPLICATION NUMBER: US 07/451,261
; PRIOR FILING DATE: 1989-12-14
; PRIOR APPLICATION NUMBER: US 371,955
; PRIOR FILING DATE: 1989-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 3522
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-825-751-7

Query Match 38.2%; Score 1408.4; DB 18; Length 3522;
Best Local Similarity 65.7%; Pred. No. 0;
Matches 2243; Conservative 0; Mismatches 1061; Indels 108; Gaps 9;

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Db        207 TGATTGGAGCTTATTTCTTTTACAGATTGAACAATTGATTGAGCAAAGAATAGAAACATT 266

Qy        345 TGCTAGGAATACGGCACTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCA 404
Db        267 GGAAAGGAACCGGGCAATTACTACATTACGAGGGTTAGCAGATAGCTATGAAATTTATAT 326

Qy        405 ACAGTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTA 464
Db        327 TGAAGCACTAAGAGAGTGGGAAGCAAATCCTAATAATGCACAATTAAGGGAAGATGTGCG 386

Qy        465 TACCCAATATATAGCCTTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAG 524
Db        387 TATTCGATTTGCTAATACAGACGACGCTTTAATAACAGCAATAAATAATTTTACACTTAC 446

Qy        525 AAACCAAGAAGTTCCATTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATT 584
Db        447 AAGTTTTGAAATCCCTCTTTTATCGGTCTATGTTCAAGCGGCGAATTTACATTTATCACT 506

Qy        585 ATTGAGAGATGCCTCTCTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACG 644
Db        507 ATTAAGAGACGCTGTATCGTTTGGGCAGGGTTGGGGACTGGATATAGCTACTGTTAATAA 566

Qy        645 TTATTATGAGCGCCAAGTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTA 704
Db        567 TCATTATAATAGATTAATAAATCTTATTCATAGATATACGAAACATTGTTTGGACACATA 626

Qy        705 TAATACAGGTCTAAATAGCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCA 764
Db        627 CAATCAAGGATTAGAAAACTTAAGAGGTACTAATACTCGACAATGGGCAAGATTCAATCA 686

Qy        765 ATTCCGTAGAGATCTAACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGA 824
Db        687 GTTTAGGAGAGATTTAACACTTACTGTATTAGATATCGTTGCTCTTTTTCCGAACTACGA 746

Qy        825 CACTCGCACTTATCCAATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGC 884
Db        747 TGTTAGAACATATCCAATTCAAACGTCATCCCAATTAACAAGGGAAATTTATACAAGTTC 806

Qy        885 AATTGGAGCAACAGGGGTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTC 944
Db        807 AGTAATTGAGGATTCTCCAGTTTCTGC----------TAATATACCTAA 845

Qy        945 GTTTTCCGCTATAGAGACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACA 1004
Db        846 TGGTTTTAATAGGGCGGAATTTGGAGTTAGACCGCCCCATCTTATGGACTTTATGAA--- 902

Qy       1005 ACTTACAATTTTTAGCACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGGCG 1064
Db        903 ---------TTCTTTGTTTGTAACTGCAGAGACTGTTAGAAGTCAAACTGTGTGGGGAGG 953

Qy       1065 GGGGCACACAATTCAATCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGTC 1124
Db        954 ACACTTAGTTAGTTCACGAAATACGGCTGGTAACCGTATAAATTTCCCTAGTTACGGGGT 1013

Qy       1125 TACCAATACTTCTATTAATCCTGTAAGATTATCATTCTTCTCTCGAGACGTATATTGGAC 1184
Db       1014 CTTCAATCCTGGTGGCGCCATTTGGATTGCAGATGAGGATCCACGTCCTTTTTATCGGAC 1073

Qy       1185 TGAATCATATGCAGGAGTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCC 1244
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Qy       1245 TACTGTTAGATTTAATTTTAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTA 1304
Db       1128 GGGGCTTAGGGGAGTAGCATTTCAACAAACTGGTACGAACCACACCCGAACATTTAGAAA 1187

Qy       1305 TAGTCAACCCTATGAGTCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACC 1364
Db       1188 TAGTGGGACCATAGATTCTCTAGATGAAATCCCACCTCAGGATAATAGTGGGGCACC-TT 1246

Qy       1365 AGAAACAACAGAACGACCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCT 1424
Db       1247 GGAATGATTATAGTCATGTATTAAATCATGTTACATTTGTACGATGGCCAGGTGAGATTT 1306
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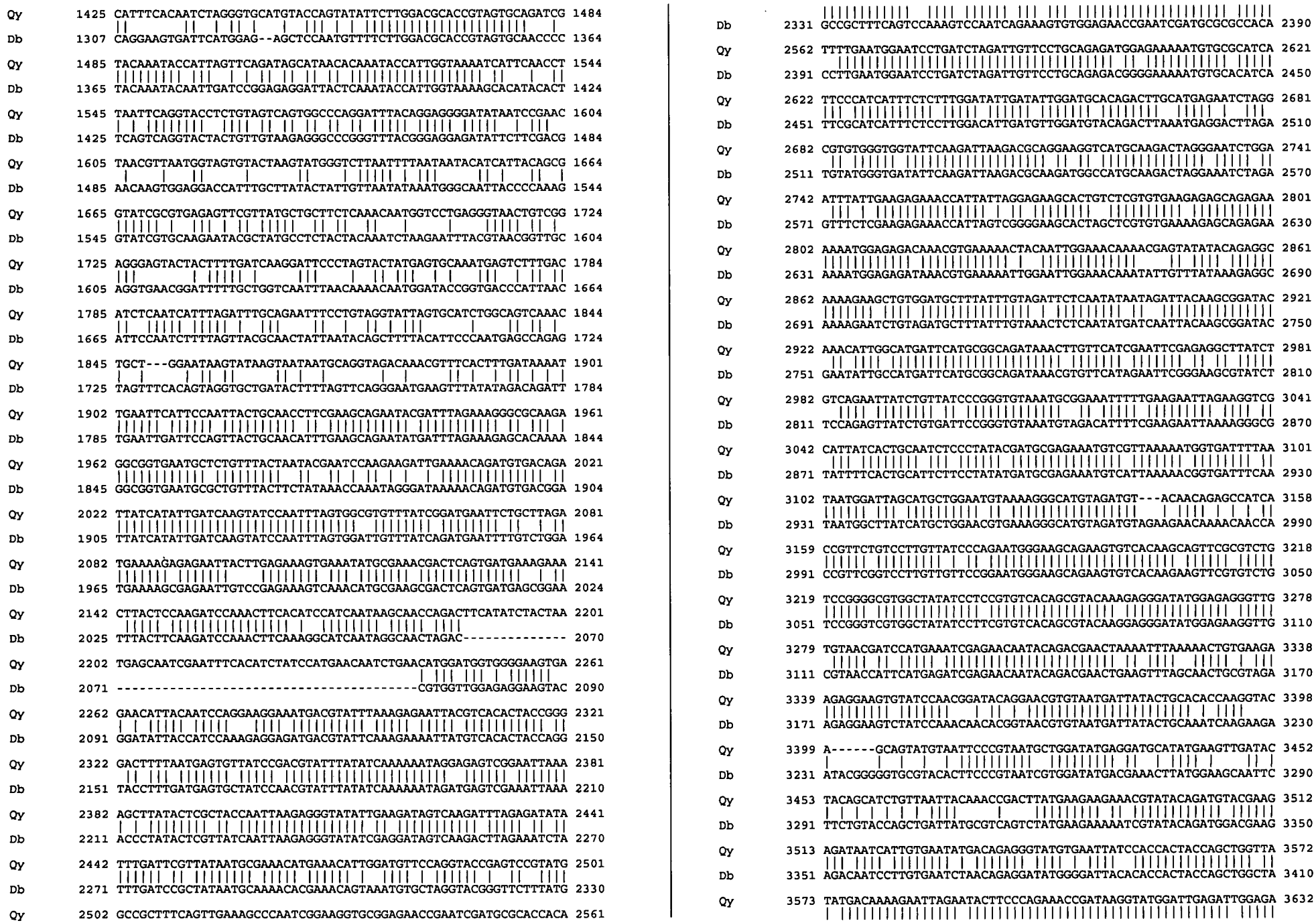

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Db        3471 AACGGAAGGAACATTCATCGTGGACAGCGTGGAATTACTCCTTATGGAGGAA 3522
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RESULT 10
US-09-873-873-25
; Sequence 25, Application US/09873873
; Patent No. US20020064865A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins
; FILE REFERENCE: MECO:210--2
; CURRENT APPLICATION NUMBER: US/09/873,873
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
;   LENGTH: 3534
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Hybrid Delta-Endotoxin
;   NAME/KEY: CDS
;   LOCATION: (1)..(3531)
US-09-873-873-25

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  Query Match             38.0%;  Score 1402;  DB 9;  Length 3534;
  Best Local Similarity   65.7%;  Pred. No. 0;
  Matches 2243;  Conservative    0;  Mismatches 1070;  Indels   99;  Gaps   10;

Qy         285 TCAGTGGGAAATTTTCCTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAA 344

Db         213 TCAATGGGACGCATTTCTTGTACAAATTGAACAGTTAATTAACCAAAGAATAGAAGAATT 272

Qy         345 TGCTAGGAATACGGCACTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCA 404

Db         273 CGCTAGGAACCAAGCCATTTCTAGATTAGAAGGACTAAGCAATCTTTATCAAATTTACGC 332

Qy         405 ACAGTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTA 464

Db         333 AGAATCTTTTAGAGAGTGGGAAGCAGATCCTACTAATCCAGCATTAAGAGAAGAGATGCG 392

Qy         465 TACCCAATATATAGCCTTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAG 524

Db         393 TATTCAATTCAATGACATGAACAGTGCCCTTACAACCGCTATTCCTCTTTTTGCAGTTCA 452

Qy         525 AAACCAAGAAGTTCCATTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATT 584

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Qy         645 TTATTATGAGCGCCAAGTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTA 704

Db         573 TCGTTATAATGATTTAACTAGGCTTATTGGCAACTATACAGATCATGCTGTACGCTGGTA 632

Qy         705 TAATACAGGTCTAAATAGCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCA 764

Db         633 CAATACGGGATTAGAGCGTGTATGGGGACCGGATTCTAGAGATTGGATAAGATATAATCA 692

Qy         765 ATTCCGTAGAGATCTAACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGA 824

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Qy         885 A--ATTGGAGCAACAGGGGTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCT 942

Db         813 AGTATTAGAAAATTTGATGGTAGTTTTCGAGGCTCGGCTCAGGGCATAGAAAGAAGTAT 872

Qy         943 TCGTTTTCCGCTATAGAGACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAA 1002

Db         873 TAGGAGTCCACATTTGATGGATATACTTAACAGTATAACCATCTATACGGATGCTCATAG 932

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Qy        1303 TATAGTCAACCCTATGAGTCACCTGGGCTTCAATTAAAAGATTCAGAAACTG-AATTACC 1361

Db        1209 AAGCGGAACGGTAGATTCGCTGGATGAAATACCGCCACAGAATAACAACGTGCCACCTAG 1268

Qy        1362 ACCAGAAACAACAGAACGACCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGG 1421

Db        1269 GCAAGGATTTAGTCATCGATTAAGCCATGTTTCAATGTTTCGT------TCAGGCTTTAG 1322

Qy        1422 GCTCATTTCACAATCTAGGGTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGA 1481

Db        1323 TAATAGTAGTGTAAGTATAATAAGAGCTCCAATGTTTTCTTGGACGCACCGTAGTGCAAC 1382

Qy        1482 TCGTACAAATACCATTAGTTCAGATAGCATAACACAAATACCATTGGTAAAATCATTCAA 1541

Db        1383 CCCTACAAATACAATTGATCCGGAGAGGATTACTCAAATACCATTGGTAAAAGCACATAC 1442

Qy        1542 CCTTAATTCAGGTACCTCTGTAGTCAGTGGCCCAGGATTTACAGGAGGGGATATAATCCG 1601

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Qy        1602 AACTAACGTTAATGGTAGTGTACTAAGTATGGGTCTTAATTTTAATAATACATCATTACA 1661

Db        1503 ACGAACAAGTGGAGGACCATTTGCTTATACTATTGTTAATATAAATGGGCAATTACCCCA 1562

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Db        1563 AAGGTATCGTGCAAGAATACGCTATGCCTCTACTACAAATCTAAGAATTTACGTAACGGT 1622

Qy        1722 CGGAGGGAGTACTACTTTTGATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTT 1781

Db        1623 TGCAGGTGAACGGATTTTTGCTGGTCAATTTAACAAAACAATGGATACCGGTGACCCATT 1682

Qy        1782 GACATCTCAATCATTTAGATTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCA 1841

Db        1683 AACATTCCAATCTTTTAGTTACGCAACTATTAATACAGCTTTTACATTCCCAATGAGCCA 1742

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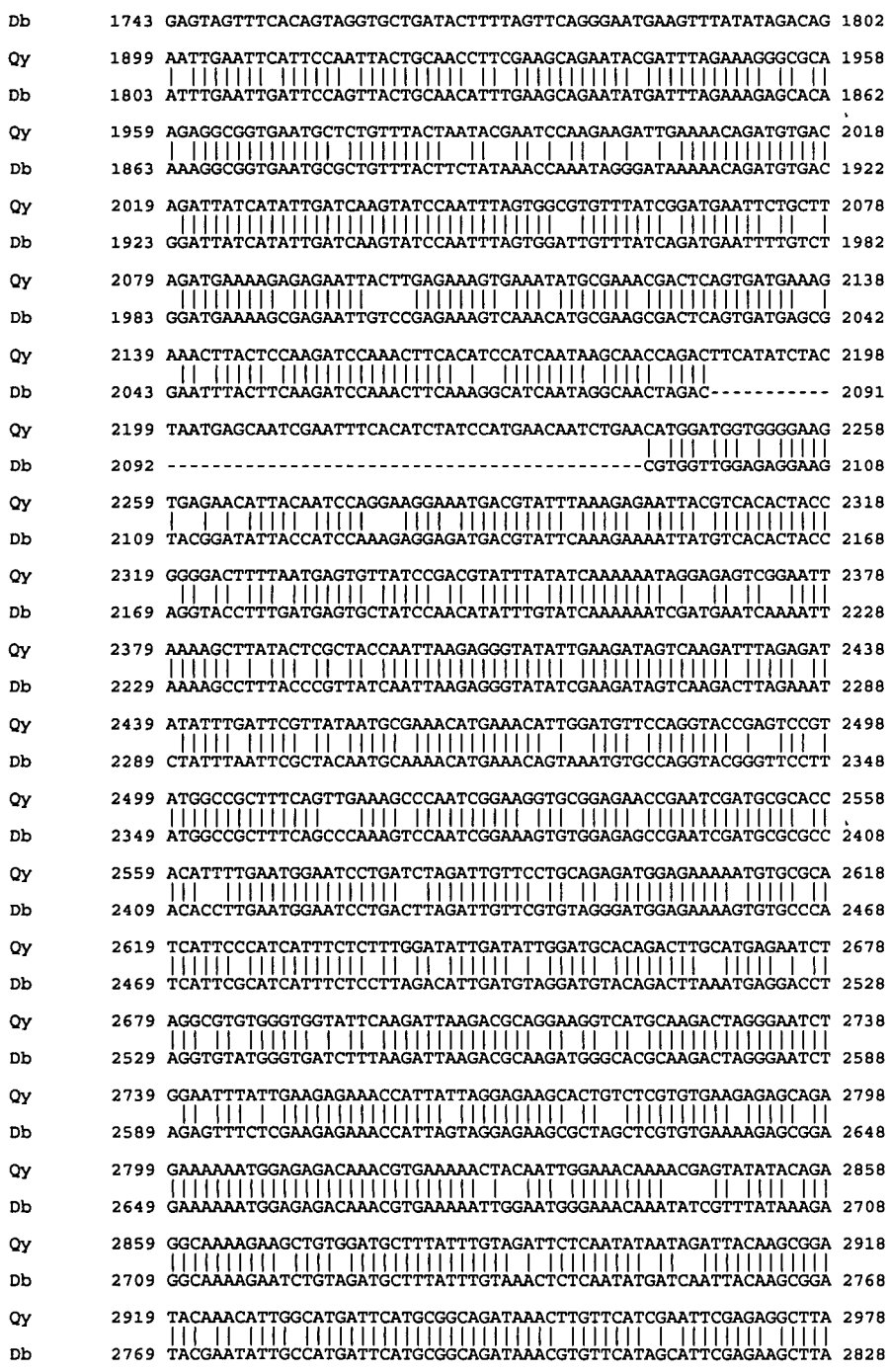

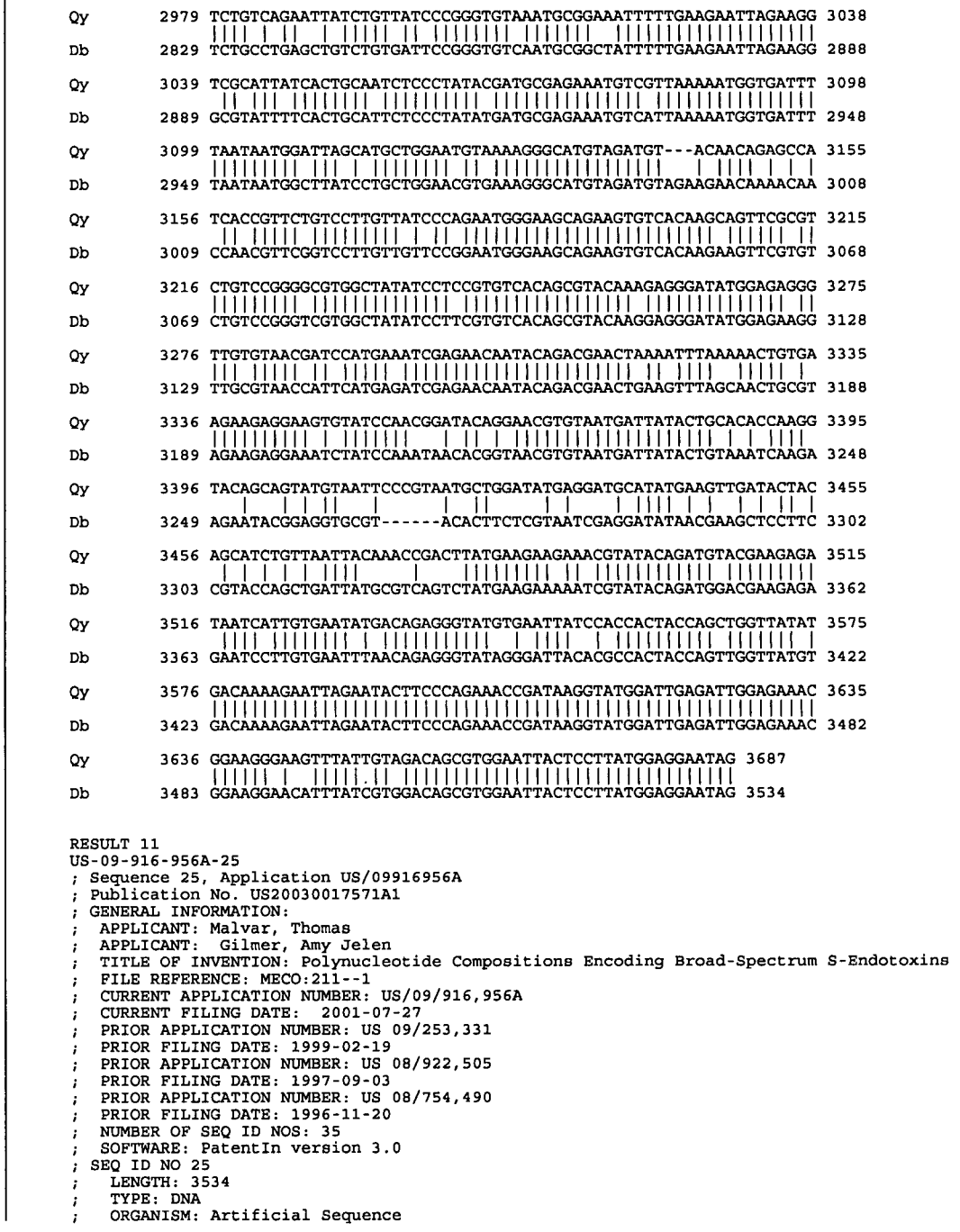

RESULT 11
US-09-916-956A-25
; Sequence 25, Application US/09916956A
; Publication No. US20030017571A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins
; FILE REFERENCE: MECO:211--1
; CURRENT APPLICATION NUMBER: US/09/916,956A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 09/253,331
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
; NAME/KEY: CDS
; LOCATION: (1)..(3531)
US-09-916-956A-25

Query Match 38.0%; Score 1402; DB 10; Length 3534;
Best Local Similarity 65.7%; Pred. No. 0;
Matches 2243; Conservative 0; Mismatches 1070; Indels 99; Gaps 10;

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Db       213 TCAATGGGACGCATTTCTTGTACAAATTGAACAGTTAATTAACCAAAGAATAGAAGAATT 272

Qy       345 TGCTAGGAATACGGCACTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCA 404
Db       273 CGCTAGGAACCAAGCCATTTCTAGATTAGAAGGACTAAGCAATCTTTATCAAATTTACGC 332

Qy       405 ACAGTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTA 464
Db       333 AGAATCTTTTAGAGAGTGGGAAGCAGATCCTACTAATCCAGCATTAAGAGAAGAGATGCG 392

Qy       465 TACCCAATATATAGCCTTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAG 524
Db       393 TATTCAATTCAATGACATGAACAGTGCCCTTACAACCGCTATTCCTCTTTTTGCAGTTCA 452

Qy       525 AAACCAAGAAGTTCCATTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATT 584
Db       453 AAATTATCAAGTTCCTCTTTTATCAGTATATGTTCAAGCTGCAAATTTACATTTATCAGT 512

Qy       585 ATTGAGAGATGCCTCTCTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACG 644
Db       513 TTTGAGAGATGTTTCAGTGTTTGGACAAAGGTGGGGATTTGATGCCGCGACTATCAATAG 572

Qy       645 TTATTATGAGCGCCAAGTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTA 704
Db       573 TCGTTATAATGATTTAACTAGGCTTATTGGCAACTATACAGATCATGCTGTACGCTGGTA 632

Qy       705 TAATACAGGTCTAAATAGCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCA 764
Db       633 CAATACGGGATTAGAGCGTGTATGGGGACCGGATTCTAGAGATTGGATAAGATATAATCA 692

Qy       765 ATTCCGTAGAGATCTAACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGA 824
Db       693 ATTTAGAAGAGAATTAACACTAACTGTATTAGATATCGTTTCTCTATTTCCGAACTATGA 752

Qy       825 CACTCGCACTTATCCAATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGC 884
Db       753 TAGTAGAACGTATCCAATTCGAACAGTTTCCCAATTAACAAGAGAAATTTATACAAACCC 812

Qy       885 A--ATTGGAGCAACAGGGGTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCT 942
Db       813 AGTATTAGAAAATTTTGATGGTAGTTTTCGAGGCTCGGCTCAGGGCATAGAAAGAAGTAT 872

Qy       943 TCGTTTTCCGCTATAGAGACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAA 1002
Db       873 TAGGAGTCCACATTTGATGGATATACTTAACAGTATAACCATCTATACGGATGCTCATAG 932

Qy      1003 CAACTTACAATTTTTAGCACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGG 1062
Db       933 GGGTTATTATTATTGGTCAGGGCATCA---------AATAATGGCTTCTCCTGTAGGGTT 983

Qy      1063 CGGGGGCACACAATTCAATCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGG 1122
Db       984 TTCGGGGCCAGAATTCACTTTTCCGCTATATGGAACTATGGGAA----------ATGCA 1032

Qy      1123 TCTACCAATACTTCTATTAATCCTGTAAGATTATCATTCTTCTCTCGAGACGTATATTGG 1182
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Qy      1183 ACTGAATCATATGCAGGAGTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTC 1242
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Qy      1243 CCTACTGTTAGATTTAATTTTAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAAC 1302
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Qy      1362 ACCAGAAACAACAGAACGACCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGG 1421
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Qy      1422 GCTCATTTCACAATCTAGGGTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGA 1481
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Qy      1482 TCGTACAAATACCATTAGTTCAGATAGCATAACACAAATACCATTGGTAAAATCATTCAA 1541
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Qy      1542 CCTTAATTCAGGTACCTCTGTAGTCAGTGGCCCAGGATTTACAGGAGGGGATATAATCCG 1601
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Qy      1662 GCGGTATCGCGTGAGAGTTCGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGT 1721
Db      1563 AAGGTATCGTGCAAGAATACGCTATGCCTCTACTACAAATCTAAGAATTTACGTAACGGT 1622

Qy      1722 CGGAGGGAGTACTACTTTTGATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTT 1781
Db      1623 TGCAGGTGAACGGATTTTTGCTGGTCAATTTAACAAAACAATGGATACCGGTGACCCATT 1682

Qy      1782 GACATCTCAATCATTTAGATTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCA 1841
Db      1683 AACATTCCAATCTTTTAGTTACGCAACTATTAATACAGCTTTTACATTCCCAATGAGCCA 1742

Qy      1842 AACTGCT---GGAATAAGTATAAGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAA 1898
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Qy      2079 AGATGAAAAGAGAGAATTACTTGAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAG 2138
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Qy      2199 TAATGAGCAATCGAATTTCACATCTATCCATGAACAATCTGAACATGGATGGTGGGGAAG 2258
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Qy       2439 ATATTTGATTCGTTATAATGCGAAACATGAAACATTGGATGTTCCAGGTACCGAGTCCGT 2498
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Qy       2499 ATGGCCGCTTTCAGTTGAAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACC 2558
Db       2349 ATGGCCGCTTTCAGCCCAAAGTCCAATCGGAAAGTGTGGAGAGCCGAATCGATGCGCGCC 2408

Qy       2559 ACATTTTGAATGGAATCCTGATCTAGATTGTTCCTGCAGAGATGGAGAAAAATGTGCGCA 2618
Db       2409 ACACCTTGAATGGAATCCTGACTTAGATTGTTCGTGTAGGGATGGAGAAAAGTGTGCCCA 2468

Qy       2619 TCATTCCCATCATTTCTCTTTGGATATTGATATTGGATGCACAGACTTGCATGAGAATCT 2678
Db       2469 TCATTCGCATCATTTCTCCTTAGACATTGATGTAGGATGTACAGACTTAAATGAGGACCT 2528

Qy       2679 AGGCGTGTGGGTGGTATTCAAGATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAATCT 2738
Db       2529 AGGTGTATGGGTGATCTTTAAGATTAAGACGCAAGATGGGCACGCAAGACTAGGGAATCT 2588

Qy       2739 GGAATTTATTGAAGAGAAACCATTATTAGGAGAAGCACTGTCTCGTGTGAAGAGAGCAGA 2798
Db       2589 AGAGTTTCTCGAAGAGAAACCATTAGTAGGAGAAGCGCTAGCTCGTGTGAAAAGAGCGGA 2648

Qy       2799 GAAAAAATGGAGAGACAAACGTGAAAAACTACAATTGGAAACAAAACGAGTATATACAGA 2858
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Qy       2859 GGCAAAAGAAGCTGTGGATGCTTTATTTGTAGATTCTCAATATAATAGATTACAAGCGGA 2918
Db       2709 GGCAAAAGAATCTGTAGATGCTTTATTTGTAAACTCTCAATATGATCAATTACAAGCGGA 2768

Qy       2919 TACAAACATTGGCATGATTCATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCTTA 2978
Db       2769 TACGAATATTGCCATGATTCATGCGGCAGATAAACGTGTTCATAGCATTCGAGAAGCTTA 2828

Qy       2979 TCTGTCAGAATTATCTGTTATCCCGGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGG 3038
Db       2829 TCTGCCTGAGCTGTCTGTGATTCCGGGTGTCAATGCGGCTATTTTTGAAGAATTAGAAGG 2888

Qy       3039 TCGCATTATCACTGCAATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTT 3098
Db       2889 GCGTATTTTCACTGCATTCTCCCTATATGATGCGAGAAATGTCATTAAAAATGGTGATTT 2948

Qy       3099 TAATAATGGATTAGCATGCTGGAATGTAAAAGGGCATGTAGATGT---ACAACAGAGCCA 3155
Db       2949 TAATAATGGCTTATCCTGCTGGAACGTGAAAGGGCATGTAGATGTAGAAGAACAAAACAA 3008

Qy       3156 TCACCGTTCTGTCCTTGTTATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGT 3215
Db       3009 CCAACGTTCGGTCCTTGTTGTTCCGGAATGGGAAGCAGAAGTGTCACAAGAAGTTCGTGT 3068

Qy       3216 CTGTCCGGGGCGTGGCTATATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGG 3275
Db       3069 CTGTCCGGGTCGTGGCTATATCCTTCGTGTCACAGCGTACAAGGAGGGATATGGAGAAGG 3128

Qy       3276 TTGTGTAACGATCCATGAAATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGA 3335
Db       3129 TTGCGTAACCATTCATGAGATCGAGAACAATACAGACGAACTGAAGTTTAGCAACTGCGT 3188

Qy       3336 AGAAGAGGAAGTGTATCCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGG 3395
Db       3189 AGAAGAGGAAATCTATCCAAATAACACGGTAACGTGTAATGATTATACTGTAAATCAAGA 3248

Qy       3396 TACAGCAGTATGTAATTCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTAC 3455

Db       3249 AGAATACGGAGGTGCGT------ACACTTCTCGTAATCGAGGATATAACGAAGCTCCTTC 3302

Qy       3456 AGCATCTGTTAATTACAAACCGACTTATGAAGAAGAAACGTATACAGATGTACGAAGAGA 3515
Db       3303 CGTACCAGCTGATTATGCGTCAGTCTATGAAGAAAAATCGTATACAGATGGACGAAGAGA 3362

Qy       3516 TAATCATTGTGAATATGACAGAGGGTATGTGAATTATCCACCACTACCAGCTGGTTATAT 3575
Db       3363 GAATCCTTGTGAATTTAACAGAGGGTATAGGGATTACACGCCACTACCAGTTGGTTATGT 3422

Qy       3576 GACAAAAGAATTAGAATACTTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGAAAC 3635
Db       3423 GACAAAAGAATTAGAATACTTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGAAAC 3482

Qy       3636 GGAAGGGAAGTTTATTGTAGACAGCGTGGAATTACTCCTTATGGAGGAATAG 3687
Db       3483 GGAAGGAACATTTATCGTGGACAGCGTGGAATTACTCCTTATGGAGGAATAG 3534
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RESULT 12
US-09-997-914-25
; Sequence 25, Application US/09997914
; Publication No. US20030119158A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad Spectrum d-Endotoxins
; FILE REFERENCE: 11792.0215.DVUS01 MECO:215--1
; CURRENT APPLICATION NUMBER: US/09/997,914
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/261,040
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
; NAME/KEY: CDS
; LOCATION: (1)..(3531)
US-09-997-914-25

Query Match 38.0%; Score 1402; DB 10; Length 3534;
Best Local Similarity 65.7%; Pred. No. 0;
Matches 2243; Conservative 0; Mismatches 1070; Indels 99; Gaps 10;

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Db        213 TCAATGGGACGCATTTCTTGTACAAATTGAACAGTTAATTAACCAAAGAATAGAAGAATT 272

Qy        345 TGCTAGGAATACGGCACTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCA 404
Db        273 CGCTAGGAACCAAGCCATTTCTAGATTAGAAGGACTAAGCAATCTTTATCAAATTTACGC 332

Qy        405 ACAGTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTA 464
Db        333 AGAATCTTTTAGAGAGTGGGAAGCAGATCCTACTAATCCAGCATTAAGAGAAGAGATGCG 392

Qy        465 TACCCAATATATAGCCTTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAG 524
Db        393 TATTCAATTCAATGACATGAACAGTGCCCTTACAACCGCTATTCCTCTTTTTGCAGTTCA 452

Qy        525 AAACCAAGAAGTTCCATTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATT 584
Db        453 AAATTATCAAGTTCCTCTTTTATCAGTATATGTTCAAGCTGCAAATTTACATTTATCAGT 512

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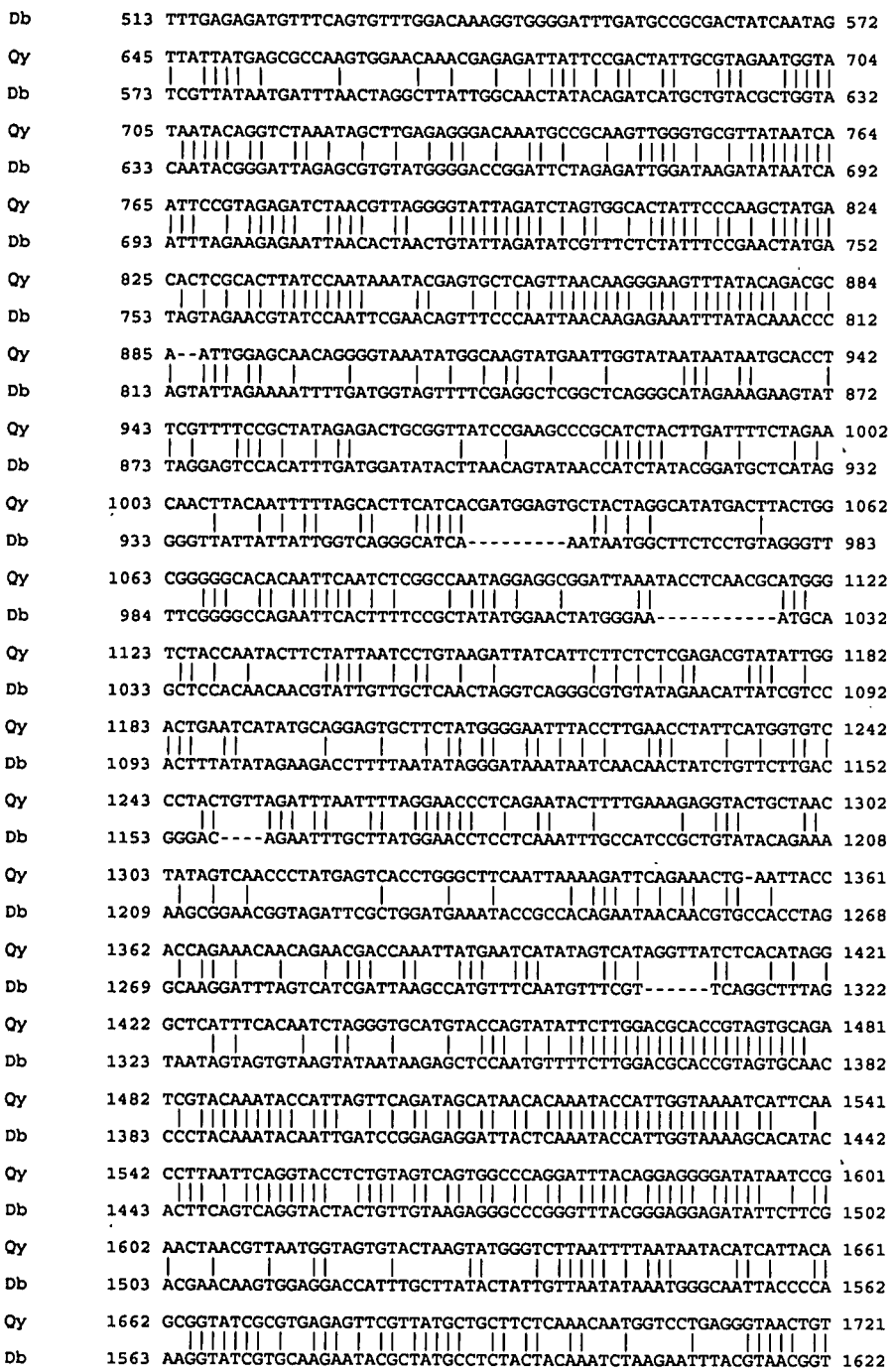

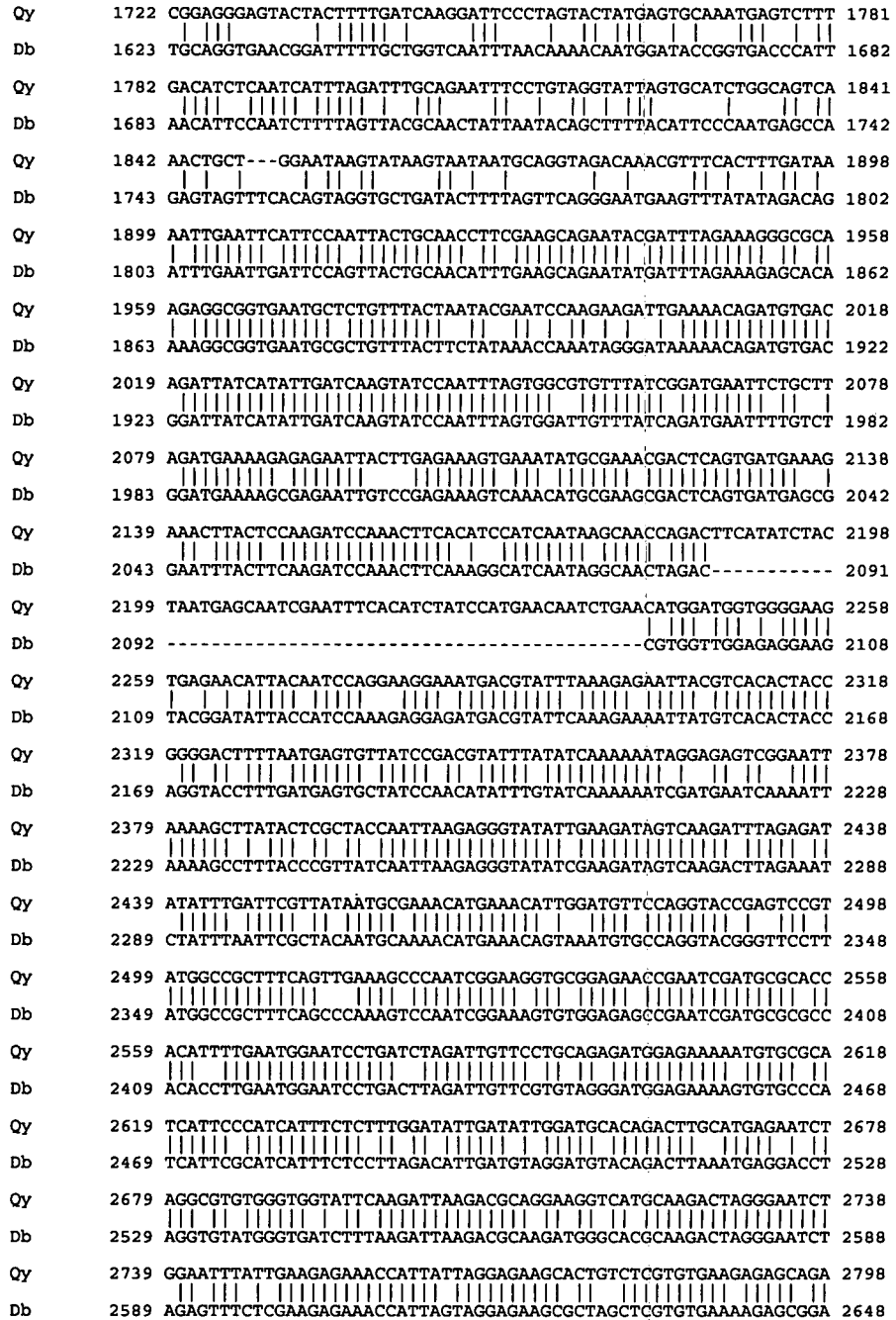

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Qy       2799 GAAAAAATGGAGAGACAAACGTGAAAAACTACAATTGGAAACAAAACGAGTATATACAGA 2858
             |||||||||||||||||||||||||||| |  ||| |||||||||     || |||| |||
Db       2649 GAAAAAATGGAGAGACAAACGTGAAAAATTGGAATGGGAAACAAATATCGTTTATAAAGA 2708

Qy       2859 GGCAAAAGAAGCTGTGGATGCTTTATTTGTAGATTCTCAATATAATAGATTACAAGCGGA 2918
             |||||||||| |||| ||||||||||||||| | |||||||||  ||  ||||||||||||
Db       2709 GGCAAAAGAATCTGTAGATGCTTTATTTGTAAACTCTCAATATGATCAATTACAAGCGGA 2768

Qy       2919 TACAAACATTGGCATGATTCATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCTTA 2978
             ||| || |||| |||||||||||||||||||||| ||||||| | |||||||| ||||
Db       2769 TACGAATATTGCCATGATTCATGCGGCAGATAAACGTGTTCATAGCATTCGAGAAGCTTA 2828

Qy       2979 TCTGTCAGAATTATCTGTTATCCCGGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGG 3038
             |||| | ||  | ||||| || |||||||| |||||||  ||||||||||||||||||||
Db       2829 TCTGCCTGAGCTGTCTGTGATTCCGGGTGTCAATGCGGCTATTTTTGAAGAATTAGAAGG 2888

Qy       3039 TCGCATTATCACTGCAATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTT 3098
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Qy       3099 TAATAATGGATTAGCATGCTGGAATGTAAAAGGGCATGTAGATGT---ACAACAGAGCCA 3155
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Db       2949 TAATAATGGCTTATCCTGCTGGAACGTGAAAGGGCATGTAGATGTAGAAGAACAAAACAA 3008

Qy       3156 TCACCGTTCTGTCCTTGTTATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGT 3215
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Db       3009 CCAACGTTCGGTCCTTGTTGTTCCGGAATGGGAAGCAGAAGTGTCACAAGAAGTTCGTGT 3068

Qy       3216 CTGTCCGGGGCGTGGCTATATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGG 3275
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Db       3069 CTGTCCGGGTCGTGGCTATATCCTTCGTGTCACAGCGTACAAGGAGGGATATGGAGAAGG 3128

Qy       3276 TTGTGTAACGATCCATGAAATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGA 3335
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Db       3129 TTGCGTAACCATTCATGAGATCGAGAACAATACAGACGAACTGAAGTTTAGCAACTGCGT 3188

Qy       3336 AGAAGAGGAAGTGTATCCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGG 3395
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Db       3189 AGAAGAGGAAATCTATCCAAATAACACGGTAACGTGTAATGATTATACTGTAAATCAAGA 3248

Qy       3396 TACAGCAGTATGTAATTCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTAC 3455
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Db       3249 AGAATACGGAGGTGCGT------ACACTTCTCGTAATCGAGGATATAACGAAGCTCCTTC 3302

Qy       3456 AGCATCTGTTAATTACAAACCGACTTATGAAGAAGAAACGTATACAGATGTACGAAGAGA 3515
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Db       3303 CGTACCAGCTGATTATGCGTCAGTCTATGAAGAAAAATCGTATACAGATGGACGAAGAGA 3362

Qy       3516 TAATCATTGTGAATATGACAGAGGGTATGTGAATTATCCACCACTACCAGCTGGTTATAT 3575
              |||| |||||||| | ||||||||||  | ||||  | |||||||||| ||||||| |
Db       3363 GAATCCTTGTGAATTTAACAGAGGGTATAGGGATTACACGCCACTACCAGTTGGTTATGT 3422

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Qy       3636 GGAAGGGAAGTTTATTGTAGACAGCGTGGAATTACTCCTTATGGAGGAATAG 3687
             |||||| |  ||||| || ||||||||||||||||||||||||||||||||
Db       3483 GGAAGGAACATTTATCGTGGACAGCGTGGAATTACTCCTTATGGAGGAATAG 3534


RESULT 13
US-10-365-645-25
; Sequence 25, Application US/10365645
; Publication No. US20030182682A1
; GENERAL INFORMATION:
;  APPLICANT: Malvar, Thomas
;  APPLICANT:  Gilmer, Amy Jelen
;  TITLE OF INVENTION: Antibodies Immunologically Reactive with Broad-Spectrum
;  TITLE OF INVENTION:  Delta-Endotoxins (Amended)
;  FILE REFERENCE: 11792.0210.DVUS02 (MECO:210--3)
;  CURRENT APPLICATION NUMBER: US/10/365,645
;  CURRENT FILING DATE:  2003-02-12
;  PRIOR APPLICATION NUMBER: US 09/873,873
;  PRIOR FILING DATE: 2001-06-04
;  PRIOR APPLICATION NUMBER: US 09/253,341
;  PRIOR FILING DATE: 1999-02-19
;  PRIOR APPLICATION NUMBER: US 08/922,505
;  PRIOR FILING DATE: 1997-09-03
;  PRIOR APPLICATION NUMBER: US 08/754,490
;  PRIOR FILING DATE: 1996-11-20
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
;  LENGTH: 3534
;  TYPE: DNA
;  ORGANISM: Artificial
;  FEATURE:
;  OTHER INFORMATION: Hybrid Delta-Endotoxin
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)..(3531)
US-10-365-645-25

  Query Match             38.0%;  Score 1402;  DB 16;  Length 3534;
  Best Local Similarity   65.7%;  Pred. No. 0;
  Matches 2243;  Conservative    0;  Mismatches 1070;  Indels   99;  Gaps   10;

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Qy        345 TGCTAGGAATACGGCACTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCA 404
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Db        273 CGCTAGGAACCAAGCCATTTCTAGATTAGAAGGACTAAGCAATCTTTATCAAATTTACGC 332

Qy        405 ACAGTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTA 464
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Db        333 AGAATCTTTTAGAGAGTGGGAAGCAGATCCTACTAATCCAGCATTAAGAGAAGAGATGCG 392

Qy        465 TACCCAATATATAGCCTTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAG 524
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Db        393 TATTCAATTCAATGACATGAACAGTGCCCTTACAACCGCTATTCCTCTTTTTGCAGTTCA 452

Qy        525 AAACCAAGAAGTTCCATTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATT 584
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Qy        645 TTATTATGAGCGCCAAGTGGAACAAACGAGAGATTATTCCGACTATTGCGTAGAATGGTA 704
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Qy        885 A--ATTGGAGCAACAGGGGTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCT 942
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Qy        943 TCGTTTTCCGCTATAGAGACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAA 1002
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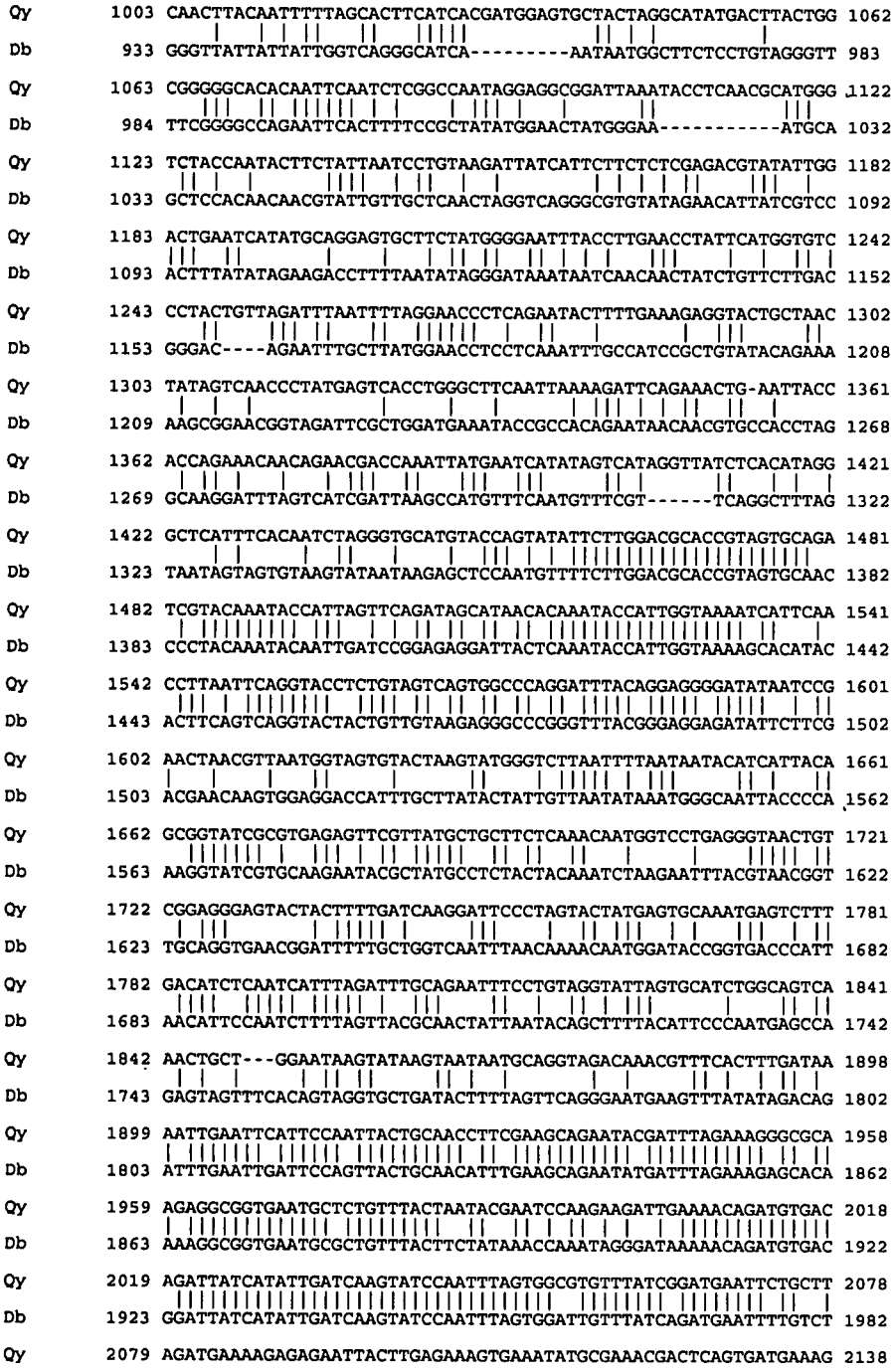

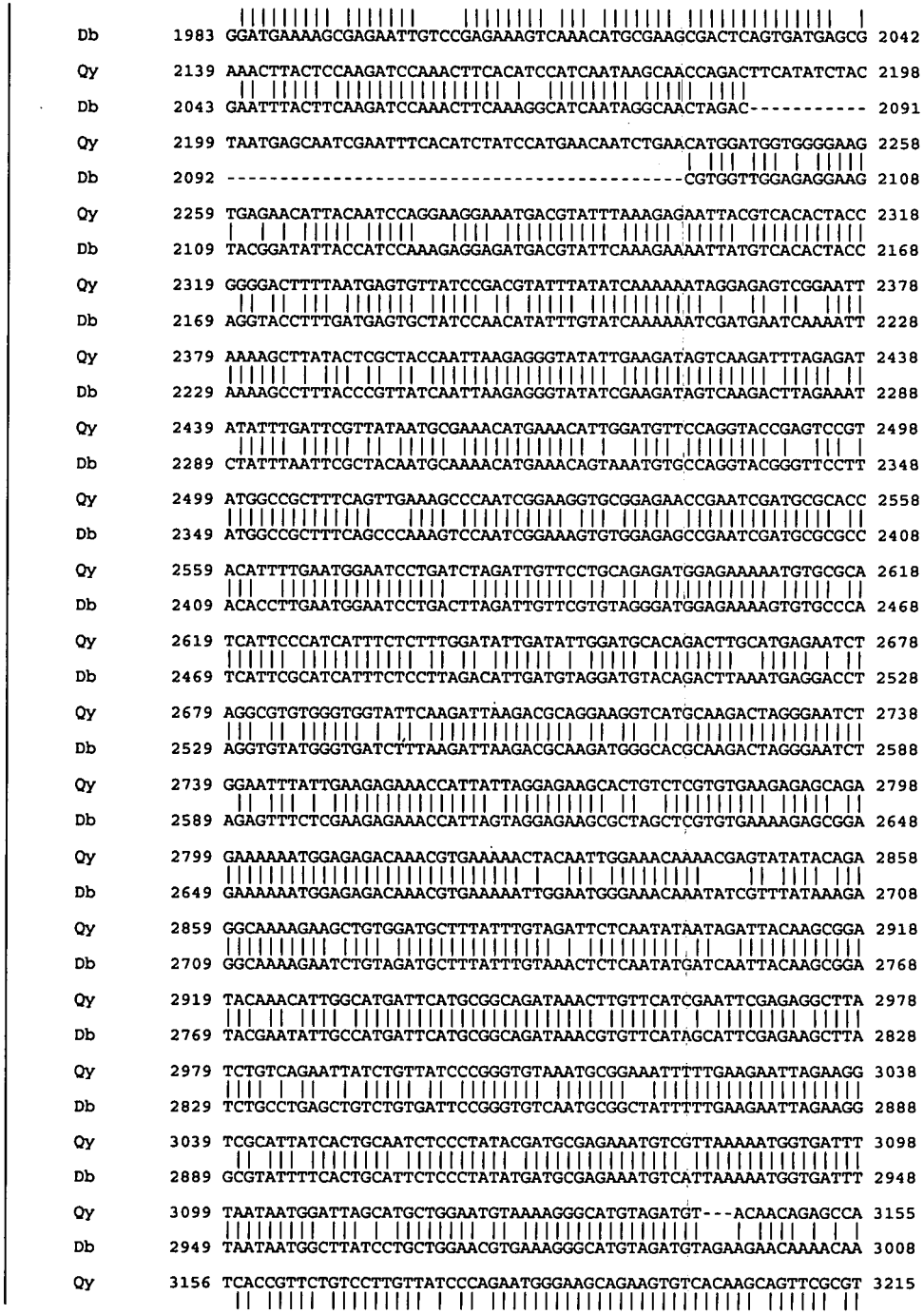

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Db       3009 CCAACGTTCGGTCCTTGTTGTTCCGGAATGGGAAGCAGAAGTGTCACAAGAAGTTCGTGT 3068

Qy       3216 CTGTCCGGGGCGTGGCTATATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGG 3275

Db       3069 CTGTCCGGGTCGTGGCTATATCCTTCGTGTCACAGCGTACAAGGAGGGATATGGAGAAGG 3128

Qy       3276 TTGTGTAACGATCCATGAAATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGA 3335

Db       3129 TTGCGTAACCATTCATGAGATCGAGAACAATACAGACGAACTGAAGTTTAGCAACTGCGT 3188

Qy       3336 AGAAGAGGAAGTGTATCCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGG 3395

Db       3189 AGAAGAGGAAATCTATCCAAATAACACGGTAACGTGTAATGATTATACTGTAAATCAAGA 3248

Qy       3396 TACAGCAGTATGTAATTCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTAC 3455

Db       3249 AGAATACGGAGGTGCGT------ACACTTCTCGTAATCGAGGATATAACGAAGCTCCTTC 3302

Qy       3456 AGCATCTGTTAATTACAAACCGACTTATGAAGAAGAAACGTATACAGATGTACGAAGAGA 3515

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Qy       3636 GGAAGGGAAGTTTATTGTAGACAGCGTGGAATTACTCCTTATGGAGGAATAG 3687

Db       3483 GGAAGGAACATTTATCGTGGACAGCGTGGAATTACTCCTTATGGAGGAATAG 3534


RESULT 14
US-10-672-163-25
; Sequence 25, Application US/10672163
; Publication No. US20040093637A1
; GENERAL INFORMATION:
;  APPLICANT: Malvar, Thomas
;  APPLICANT:  Gilmer, Amy Jelen
;  TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad Spectrum
;  TITLE OF INVENTION:  delta-Endotoxins
;  FILE REFERENCE: 11792.0215.DVUS02   MECO:215--2
;  CURRENT APPLICATION NUMBER: US/10/672,163
;  CURRENT FILING DATE:  2003-09-26
;  PRIOR APPLICATION NUMBER: US 09/997,914
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: US 09/261,040
;  PRIOR FILING DATE: 1999-03-02
;  PRIOR APPLICATION NUMBER: US 08/754,490
;  PRIOR FILING DATE: 1996-11-20
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
;   LENGTH: 3534
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Hybrid Delta-Endotoxin
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3531)
US-10-672-163-25

  Query Match           38.0%;  Score 1402;  DB 17;  Length 3534;
  Best Local Similarity   65.7%;  Pred. No. 0;
  Matches 2243;  Conservative    0;  Mismatches 1070;  Indels   99;  Gaps   10;

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Qy        345 TGCTAGGAATACGGCACTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCA 404

Db        273 CGCTAGGAACCAAGCCATTTCTAGATTAGAAGGACTAAGCAATCTTTATCAAATTTACGC 332

Qy        405 ACAGTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTA 464

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Qy        465 TACCCAATATATAGCCTTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAG 524

Db        393 TATTCAATTCAATGACATGAACAGTGCCCTTACAACCGCTATTCCTCTTTTTGCAGTTCA 452

Qy        525 AAACCAAGAAGTTCCATTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATT 584

Db        453 AAATTATCAAGTTCCTCTTTTATCAGTATATGTTCAAGCTGCAAATTTACATTTATCAGT 512

Qy        585 ATTGAGAGATGCCTCTCTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACG 644

Db        513 TTTGAGAGATGTTTCAGTGTTTGGACAAAGGTGGGGATTTGATGCCGCGACTATCAATAG 572

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Qy        705 TAATACAGGTCTAAATAGCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCA 764

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Db        693 ATTTAGAAGAGAATTAACACTAACTGTATTAGATATCGTTTCTCTATTTCCGAACTATGA 752

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Qy       1063 CGGGGGCACACAATTCAATCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGG 1122

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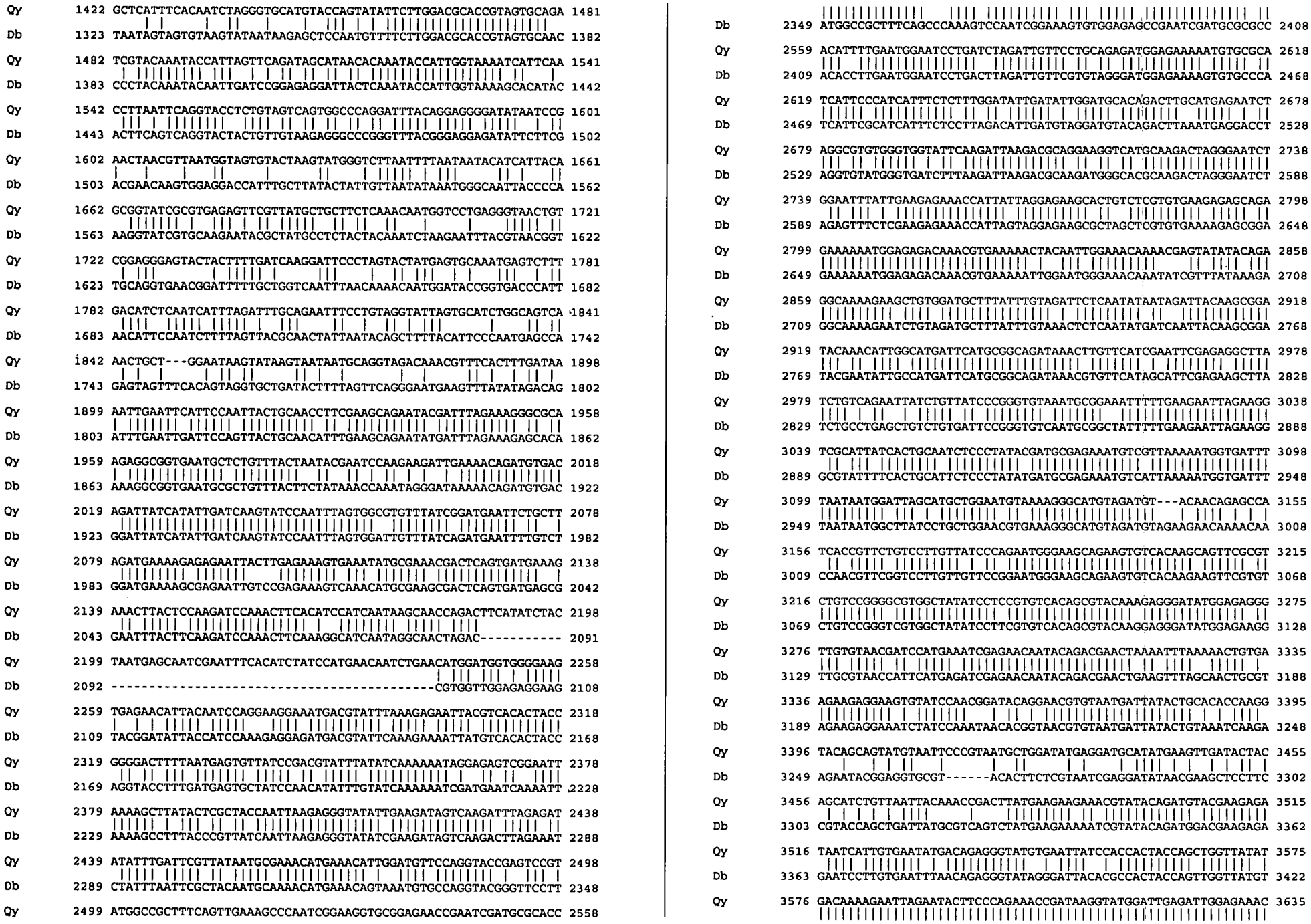

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RESULT 15
US-10-739-482-25
; Sequence 25, Application US/10739482
; Publication No. US20040132975A1
; GENERAL INFORMATION:
;  APPLICANT: Malvar, Thomas
;  APPLICANT:  Mohan, Komarlingham S.
;  APPLICANT:  Sivasupramaniam, Sakuntala
;  TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad Spectrum
;  TITLE OF INVENTION:  Delta-Endotoxins
;  FILE REFERENCE: MECO:220--1
;  CURRENT APPLICATION NUMBER: US/10/739,482
;  CURRENT FILING DATE:  2003-12-18
;  PRIOR APPLICATION NUMBER: US 09/636,746
;  PRIOR FILING DATE: 2000-08-11
;  PRIOR APPLICATION NUMBER: US 6,242,241
;  PRIOR FILING DATE: 1999-02-19
;  PRIOR APPLICATION NUMBER: US 6,110,464
;  PRIOR FILING DATE: 1997-09-03
;  PRIOR APPLICATION NUMBER: US 6,017,534
;  PRIOR FILING DATE: 1996-11-20
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
;   LENGTH: 3534
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Hybrid Delta-Endotoxin
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3531)
US-10-739-482-25

  Query Match             38.0%;  Score 1402;  DB 18;  Length 3534;
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  Matches 2243;  Conservative    0;  Mismatches 1070;  Indels   99;  Gaps   10;

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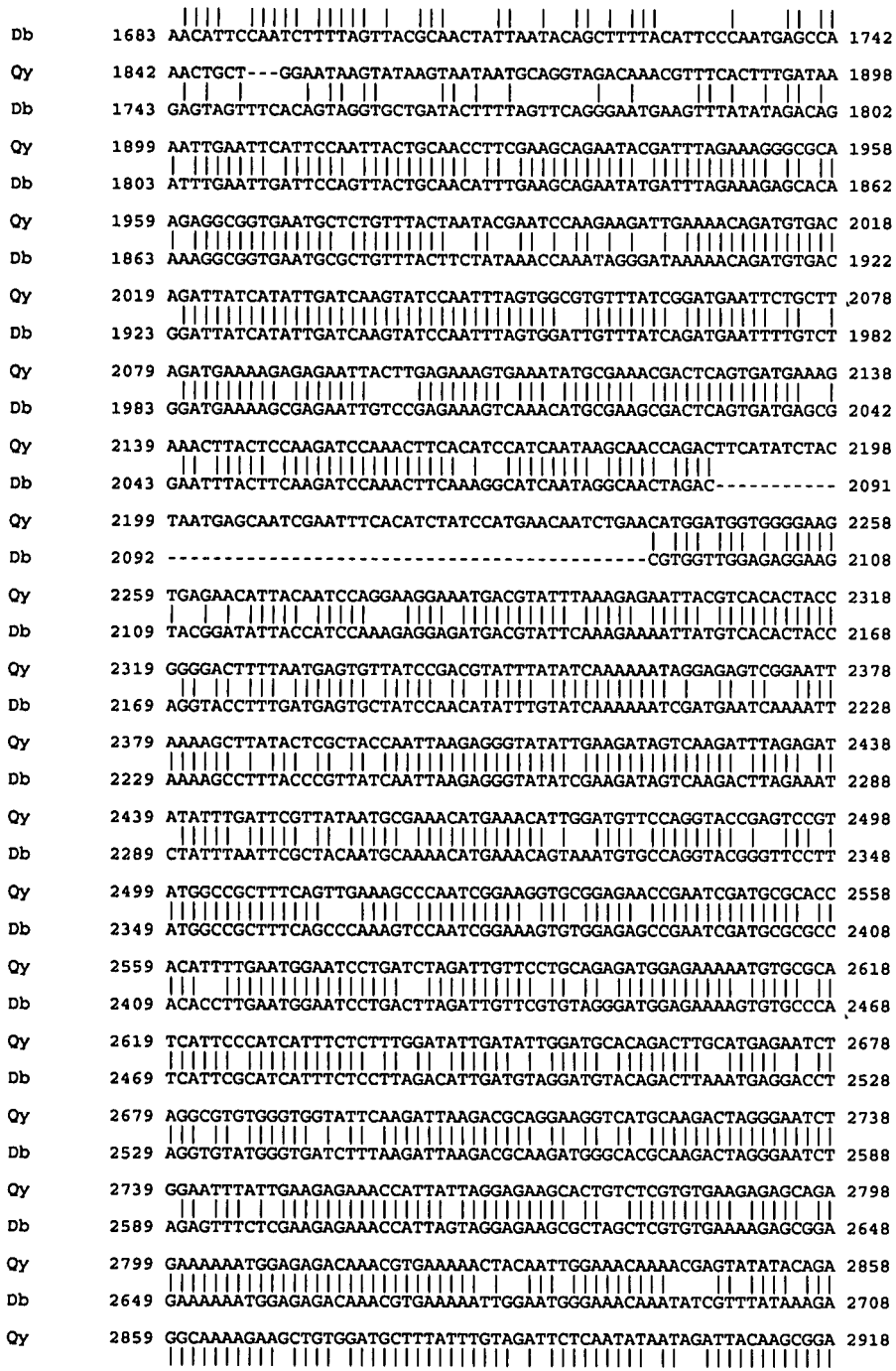

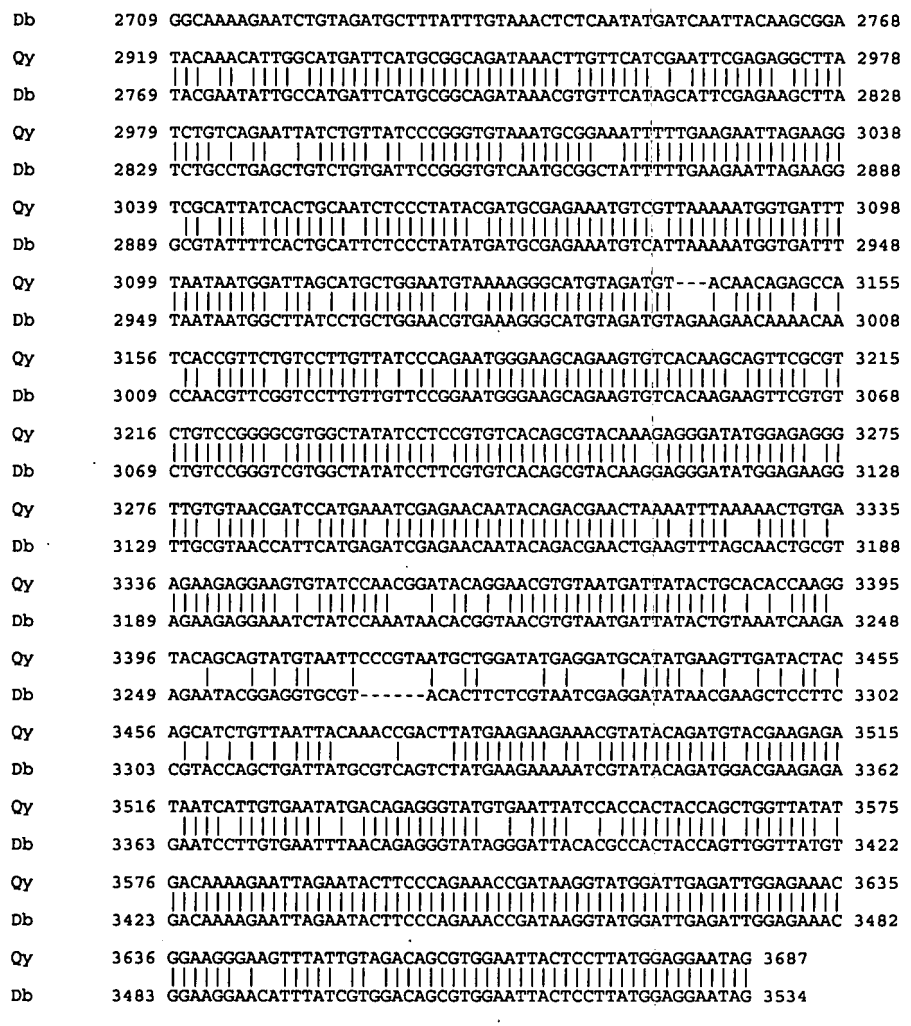

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Job time : 2035 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 24, 2005, 14:00:19 ; Search time 46 Seconds
(without alignments)
1992.805 Million cell updates/sec

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Perfect score: 6479
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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20	5108	78.8	1186	4	US-09-826-660-23	Sequence 23, Appl
21	3977.5	61.4	1174	1	US-08-040-751-3	Sequence 3, Appli
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23	3977.5	61.4	1174	2	US-08-962-190-2	Sequence 2, Appli
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ALIGNMENTS

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; Sequence 38, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-661-322A-38

Query Match 99.7%; Score 6462; DB 4; Length 1228;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1223; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db        961 LFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITAIS 1020

Qy       1021 LYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYIL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 LYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYIL 1080

Qy       1081 RVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAVCNSRN 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db       1081 RVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAACNSRN 1140

Qy       1141 AGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEYFP 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db       1141 AGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYVTKELEYFP 1200

Qy       1201 ETDKVWIEIGETEGKFIVDSVELLLMEE 1228
              |||||||||||||| |||||:|||||||
Db       1201 ETDKVWIEIGETEGTFIVDSIELLLMEE 1228
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RESULT 2
US-08-448-170-8
; Sequence 8, Application US/08448170
; Patent No. 5723758
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-448-170-8

Query Match 91.5%; Score 5926.5; DB 1; Length 1227;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1129; Conservative 36; Mismatches 60; Indels 5; Gaps 3;

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Qy          1 LTSNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
              |||||||||||||||||||||||| ||:|| |||||||||||||||:| ||||||||||
Db          1 LTSNRKNENEIINALSIPAVSNHSAQMNLSTDARIEDSLCIAEGNNIDPFVSASTVQTGI 60

Qy         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 120
              |||||||||||||||||||||||||||||||| |||||||||| ||:||| |:||
Db         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDPWEIFLEHVEQLIRQQVTENTRDTA 120

Qy        121 LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 180
              ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LARLQGLGNSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 180

Qy        181 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLN 240
              |||||||||||||||||||||||||||||||||||||||||||:||:|||||  |||||||
Db        181 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEKTREYSDYCARWYNTGLN 240

Qy        241 SLRGTNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG 300
              :|||||| ||:|||||||||||||||||||||||| ||:|||||||||:||| || |
Db        241 NLRGTNAESWLRYNQFRRDLTLGVLDLVALFPSYDTRVYPMNTSAQLTREIYTDPIGRTN 300

Qy        301 V--NMASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHT 358
                  || ||:|||||||||||| |||| |||||| ||||||| |||| |::| || ||
Db        301 APSGFASTNWFNNNAPSFSAIEAAVIRPPHLLDFPEQLTIFSVLSRWSNTQYMNYWVGHR 360

Qy        359 IQSRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTVR 418
              ::|| | | |:|||||:|||||||| | | ||||| |||:||: : :   |::|||  |
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Db        361 LESRTIRGSLSTSTHGNTNTSINPVTLQFTSRDVYRTESFAGINI--LLTTPVNGVPWAR 418

Qy        419 FNFRNPQNTFERGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLISQ 478
              ||:||| |:  ||:  |:  |   | || |||||||||||||||||||||:| |||
Db        419 FNWRNPLNSL-RGSLLYTIGYTGVGTQLFDSETELPPETTERPNYESYSHRLSNIRLISG 477

Qy        479 SRVHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVN 538
              : :  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 NTLRAPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVN 537

Qy        539 GSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQS 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 GSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQS 597

Qy        599 FRFAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNA 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 FRFAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNA 657

Qy        659 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 718
              |||||||||||| |||||||:||||||||||||||||||||||||||||||||||||||
Db        658 LFTNTNPRRLKTGVTDYHIDEVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 717

Qy        719 PNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNE 778
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        718 PNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVILPGTFNE 777

Qy        779 CYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSV 838
              ||||||||||||:|||||||||| ||||||||||||||||||||||||||||||||||||
Db        778 CYPTYLYQKIGEAELKAYTRYQLSGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSV 837

Qy        839 ESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVV 898
              ||||||||||||||||||||||||||||||||||||||||||:|| ||||||||||||
Db        838 ESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDVGCIDLHENLGVWVV 897

Qy        899 FKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAV 958
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 FKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAV 957

Qy        959 DALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITA 1018
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 DALFVDSQYDRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITA 1017

Qy       1019 ISLYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGY 1078
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 ISLYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGY 1077

Qy       1079 ILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAVCNS 1138
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       1078 ILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAACNS 1137

Qy       1139 RNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEY 1198
              ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db       1138 RNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPVPAGYMTKELEY 1197

Qy       1199 FPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
              |||||||||||||||||||||||||||||
Db       1198 FPETDKVWIEIGETEGKFIVDSVELLLMEE 1227


RESULT 3
US-08-961-803-9
; Sequence 9, Application US/08961803
; Patent No. 6150589
;  GENERAL INFORMATION:
;    APPLICANT:  Payne, Jewel
;    APPLICANT:  Cummings, David A.
;    APPLICANT:  Cannon, Raymond J.C.
;    APPLICANT:  Narva, Kenneth E.
;    APPLICANT:  Stelman, Steve
;    TITLE OF INVENTION:  No. 6150589el Bacillus thuringiensis Isolate Denoted
;    TITLE OF INVENTION:  B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
;    TITLE OF INVENTION:  Encoding Lepidopteran-Active Toxins
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jay M. Sanders
;      STREET:  2421 N.W. 41st Street, Suite A-1
;      CITY:  Gainesville
;      STATE:  Florida
;      COUNTRY:  USA
;      ZIP:  32606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/961,803
;      FILING DATE:  31-OCT-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/069,902
;      FILING DATE:  01-JUNE-1993
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/759,247
;      FILING DATE:  13-SEPT-1991
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/448,170
;      FILING DATE:  23-MAY-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sanders, Jay M.
;      REGISTRATION NUMBER:  39,355
;      REFERENCE/DOCKET NUMBER:  M/S 102DCD1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (352) 375-8100
;      TELEFAX:  (352) 372-5800
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1227 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-961-803-9

  Query Match             91.5%;  Score 5926.5;  DB 3;  Length 1227;
  Best Local Similarity   91.8%;  Pred. No. 0;
  Matches 1129;  Conservative   36;  Mismatches   60;  Indels    5;  Gaps    3;

Qy          1 LTSNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
              |||||||||||||||||||||||||||||| ||:|| |||||||||||||||:| ||||||||||
Db          1 LTSNRKNENEIINALSIPAVSNHSAQMNLSTDARIEDSLCIAEGNNIDPFVSASTVQTGI 60

Qy         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 120
              |||||||||||||||||||||||||||||||||||| |||||||||| ||:||| |:||
Db         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDPWEIFLEHVEQLIRQQVTENTRDTA 120

Qy        121 LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 180
              ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LARLQGLGNSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 180

Qy        181 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLN 240
              |||||||||||||||||||||||||||||||||||||||||:||:|||||  |||||||
Db        181 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEKTREYSDYCARWYNTGLN 240

Qy        241 SLRGTNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG 300
              :|||||  ||:|||||||||||||||||||||||||||  ||:|||||||:||| || |
Db        241 NLRGTNAESWLRYNQFRRDLTLGVLDLVALFPSYDTRVYPMNTSAQLTREIYTDPIGRTN 300

Qy        301 V--NMASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHT 358
                  || ||:|||||||||||| |||| |||||| ||||||  |||| |::| || ||
Db        301 APSGFASTNWFNNNAPSFSAIEAAVIRPPHLLDFPEQLTIFSVLSRWSNTQYMNYWVGHR 360

Qy        359 IQSRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTVR 418
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Db        361 LESRTIRGSLSTSTHGNTNTSINPVTLQFTSRDVYRTESFAGINI--LLTTPVNGVPWAR 418

Qy        419 FNFRNPQNTFERGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLISQ 478

Db        419 FNWRNPLNSL-RGSLLYTIGYTGVGTQLFDSETELPPETTERPNYESYSHRLSNIRLISG 477

Qy        479 SRVHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVN 538

Db        478 NTLRAPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVN 537

Qy        539 GSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQS 598

Db        538 GSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQS 597

Qy        599 FRFAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNA 658

Db        598 FRFAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNA 657

Qy        659 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 718

Db        658 LFTNTNPRRLKTGVTDYHIDEVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 717

Qy        719 PNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNE 778

Db        718 PNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVILPGTFNE 777

Qy        779 CYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSV 838

Db        778 CYPTYLYQKIGEAELKAYTRYQLSGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSV 837

Qy        839 ESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVV 898

Db        838 ESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDVGCIDLHENLGVWVV 897

Qy        899 FKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAV 958

Db        898 FKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAV 957

Qy        959 DALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITA 1018

Db        958 DALFVDSQYDRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITA 1017

Qy       1019 ISLYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGY 1078

Db       1018 ISLYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGY 1077

Qy       1079 ILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAVCNS 1138

Db       1078 ILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAACNS 1137

Qy       1139 RNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEY 1198

Db       1138 RNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPVPAGYMTKELEY 1197

Qy       1199 FPETDKVWIEIGETEGKFIVDSVELLLMEE 1228

Db       1198 FPETDKVWIEIGETEGKFIVDSVELLLMEE 1227


RESULT 4
US-09-661-322A-63
; Sequence 63, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
;  APPLICANT: Baum, James A.
;  APPLICANT:  Chu, Chih-Rei
;  APPLICANT:  Donovan, William P.
;  APPLICANT:  Gilmer, Amy J.
;  APPLICANT:  Rupar, Mark J.
;  TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
;  TITLE OF INVENTION:  and Methods of Use
;  FILE REFERENCE: MECO201
;  CURRENT APPLICATION NUMBER: US/09/661,322A
;  CURRENT FILING DATE:  2000-09-13
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63
;   LENGTH: 1227
;   TYPE: PRT
;   ORGANISM: Bacillus thuringiensis
US-09-661-322A-63

  Query Match             91.3%;  Score 5912.5;  DB 4;  Length 1227;
  Best Local Similarity   91.6%;  Pred. No. 0;
  Matches 1127;  Conservative   36;  Mismatches   62;  Indels    5;  Gaps    3;

Qy          1 LTSNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60

Db          1 LTSNRKNENEIINALSIPAVSNHSAQMNLSTDARIEDSLCIAEGNNIDPFVSASTVQTGI 60

Qy         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 120

Db         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDPWEIFLEHVEHLIRQQVTENTRDTA 120

Qy        121 LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 180

Db        121 LARLQGLGNSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 180

Qy        181 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLN 240

Db        181 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEKTREYSDYCARWYNTGLN 240

Qy        241 SLRGTNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG 300

Db        241 NLRGTNAESWLRYNQFRRDLTLGVLDLVALFPSYDTRVYPMNTSAQLTREIYTDPIGRTN 300

Qy        301 V--NMASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHT 358

Db        301 APSGFASTNWFNNNAPSFSAIEAAVIRPPHLLDFPEQLTIFSVLSRWSNTQYMNYWVGHR 360

Qy        359 IQSRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTVR 418

Db        361 LESRTIRGSLSTWTHGNTNTSINPVTLQFTSRDVYRTESFAGINI--LLTTPVNGVPWAR 418

Qy        419 FNFRNPQNTFERGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLISQ 478

Db        419 FNWRNPLNSL-RGSLLYTIGYTGVGTQLFDSETELPPETTERPNYESYSHRLSNIRLISG 477

Qy        479 SRVHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVN 538

Db        478 NTLRAPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVN 537

Qy        539 GSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQS 598

Db        538 GSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQS 597

Qy        599 FRFAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNA 658

Db        598 FRFAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNA 657

Qy        659 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 718

Db        658 LFTNTNPRRLKTGVTDYHIDEVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 717

Qy        719 PNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNE 778

Db        718 PNFTSINKQPDFNSNNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNE 777

Qy        779 CYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSV 838

Db        778 CYPTYLYQKIGEAELKAYTRYQLSGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSV 837

Qy        839 ESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVV 898

Db        838 ESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDVGCIDLHENLGVWVV 897
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Qy        899 FKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAV 958
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 FKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAV 957

Qy        959 DALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITA 1018
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 DALFVDSQYDRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITA 1017

Qy       1019 ISLYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGY 1078
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 ISLYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGY 1077

Qy       1079 ILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAVCNS 1138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 ILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAVCNS 1137

Qy       1139 RNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEY 1198
              ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db       1138 RNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPVPAGYMTKELEY 1197

Qy       1199 FPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
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Db       1198 FPETDKVWIEIGETEGKFIVDSVELLLMEE 1227


RESULT 5
US-07-951-715A-7
; Sequence 7, Application US/07951715A
; Patent No. 5625136
;  GENERAL INFORMATION:
;    APPLICANT:  Koziel, Michael G.
;    APPLICANT:  Desai, Nalini M.
;    APPLICANT:  Lewis, Kelly S.
;    APPLICANT:  Kramer, Vance C.
;    APPLICANT:  Warren, Gregory W.
;    APPLICANT:  Evola, Stephen V.
;    APPLICANT:  Crossland, Lyle D.
;    APPLICANT:  Wright, Martha S.
;    APPLICANT:  Merlin, Ellis J.
;    APPLICANT:  Launis, Karen L.
;    APPLICANT:  Rothstein, Steven J.
;    APPLICANT:  Bowman, Cindy G.
;    APPLICANT:  Dawson, John L.
;    APPLICANT:  Dunder, Erik M.
;    APPLICANT:  Pace, Gary M.
;    APPLICANT:  Suttie, Janet L.
;    TITLE OF INVENTION:  SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;    TITLE OF INVENTION:  INSECTICIDAL ACTIVITY IN MAIZE
;    NUMBER OF SEQUENCES:  94
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CIBA-GEIGY Corporation
;      STREET:  7 Skyline Drive
;      CITY:  Hawthorne
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10532
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/951,715A
;      FILING DATE:  25-SEP-1992
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/772,027
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spruill, W. Murray
;      REGISTRATION NUMBER:  32,943
;      REFERENCE/DOCKET NUMBER:  S-18805/A/CGC 1577/CIP
;      TELECOMMUNICATION INFORMATION:
;        TELEPHONE:  (919)541-8615
;        TELEFAX:  (919)541-8689
;    INFORMATION FOR SEQ ID NO:  7:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH:  1207 amino acids
;        TYPE:  amino acid
;        TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
US-07-951-715A-7

  Query Match             87.4%;  Score 5659.5;  DB 1;  Length 1207;
  Best Local Similarity   89.4%;  Pred. No. 0;
  Matches 1079;  Conservative   34;  Mismatches   89;  Indels    5;  Gaps    2;

Qy         27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRILGVLGVPFAGQIASFYSFLV 86
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Db          1 MDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLV 60

Qy         87 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 120

Qy        147 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 180

Qy        207 GLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 266
              ||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLTSQEIQRYYERQVERTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 240

Qy        267 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIETAVIRS 326
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        241 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIEAAAIRS 300

Qy        327 PHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPIGGGLNTSTHGSTNTSINPVRLS 386
              |||||||||||||| ||||| ||||||||||||||||||||||:|||||||| |
Db        301 PHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLR 360

Qy        387 FFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFNFRNPQNTFERGTANYSQPYESPGLQL 446
              | ||||| |||||||||||||||||||||||||||| ||||  :|||||||||||||||||
Db        361 FASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNISDRGTANYSQPYESPGLQL 420

Qy        447 KDSETELPPETTERPNYESYSHRLSHIGLISQSRVHVPVYSWTHRSADRTNTISSDSITQ 506
              |||||||||||||||||||||||||||:| ||||:|||||||||||||||  : |||
Db        421 KDSETELPPETTERPNYESYSHRLSHIGIILQSRVNVPVYSWTHRSADRTNTIGPNRITQ 480

Qy        507 IPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ 566
              ||:||:  |  ||:|| |||||||||:|    |    : :  |    ||||:  |||::
Db        481 IPMVKASELPQGTTVVRGPGFTGGDILRRTNTGGFGPIRVTVNGPLTQRYRIGFRYASTV 540

Qy        567 TMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFRFAEFPVGISASGSQ-TAGISISNNAG 625
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Db        541 DFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTTPFTFTQIQDIIRTSIQGLSG 600

Qy        626 RQTFHFDKIEFIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 685
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Db        601 NGEVYIDKIEIIPVTATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 660

Qy        686 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 720

Qy        746 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 780

Qy        806 EDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 865
              |||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db        781 EDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 840

Qy        866 RDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 925
              |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
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Db        841 RDGEKCAHHSHHFSLDIDVGCTDLHENLGVWVVPKIKTQEGHARLGNLEFIEEKPLLGEA 900

Qy        926 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKL 985
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Db        901 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHAADKL 960

Qy        986 VHRIREAYLSELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGH 1045
              |||||||||||| |||||||||||||| |||||||||||||||||||| |||||||
Db        961 VHRIREAYLSELPVIPGVNAEIFEELEGHIITAISLYDARNVVKNGDFNNGLTCWNVKGH 1020

Qy       1046 VDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDE 1105
              |||||||||| |||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1021 VDVQQSHHRSDLVIPEWEAEVSQAVRVCPGCGYILRVTAYKEGYGEGCVTIHEIENNTDE 1080

Qy       1106 LKFKNCEEEEVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAYEVDTTASVNYKPTY 1161
              ||||| |||||||||||||||||||||     ||||||||||||||||||||||||||||
Db       1081 LKFKNREEEEVYPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVNYKPTY 1140

Qy       1162 EEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSV 1221
              ||||||||||||||||||||||||:||||:|||||||||| ||||||||||||||||||
Db       1141 EEETYTDVRRDNHCEYDRGYVNYPPVPAGYVTKELEYFPETDTVWIEIGETEGKFIVDSV 1200

Qy       1222 ELLLMEE 1228
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Db       1201 ELLLMEE 1207


RESULT 6
US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
;  GENERAL INFORMATION:
;    APPLICANT:  Koziel, Michael G.
;    APPLICANT:  Desai, Nalini M.
;    APPLICANT:  Lewis, Kelly S.
;    APPLICANT:  Kramer, Vance C.
;    APPLICANT:  Warren, Gregory W.
;    APPLICANT:  Evola, Stephen V.
;    APPLICANT:  Crossland, Lyle D.
;    APPLICANT:  Wright, Martha S.
;    APPLICANT:  Merlin, Ellis J.
;    APPLICANT:  Launis, Karen L.
;    APPLICANT:  Rothstein, Steven J.
;    APPLICANT:  Bowman, Cindy G.
;    APPLICANT:  Dawson, John L.
;    APPLICANT:  Dunder, Erik M.
;    APPLICANT:  Pace, Gary M.
;    APPLICANT:  Suttie, Janet L.
;    TITLE OF INVENTION:  SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;    TITLE OF INVENTION:  INSECTICIDAL ACTIVITY IN MAIZE
;    NUMBER OF SEQUENCES:  94
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 5859336artis Corporation
;      STREET:  Patent & Trademark Dept., 520 White Plains
;      STREET:  Rd., POB 2005
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10591-9005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,448A
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,715
;      FILING DATE:  25-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/772,027
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pace, Gary M.
;      REGISTRATION NUMBER:  40403
;      REFERENCE/DOCKET NUMBER:  CGC 1577/CIP/DIV4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)541-8582
;      TELEFAX:  (919)541-8689
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1207 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-459-448A-7

  Query Match             87.4%;  Score 5659.5;  DB 2;  Length 1207;
  Best Local Similarity   89.4%;  Pred. No. 0;
  Matches 1079;  Conservative   34;  Mismatches   89;  Indels    5;  Gaps    2;

Qy          27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRILGVLGVPFAGQIASFYSFLV 86
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Db           1 MDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLV 60

Qy          87 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 146
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Db          61 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 120

Qy         147 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 206
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Db         121 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 180

Qy         207 GLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 266
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Db         181 GLTSQEIQRYYERQVERTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 240

Qy         267 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIETAVIRS 326
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Db         241 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIEAAAIRS 300

Qy         327 PHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPIGGGLNTSTHGSTNTSINPVRLS 386
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Db         301 PHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLR 360

Qy         387 FFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFNFRNPQNTFERGTANYSQPYESPGLQL 446
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Db         361 FASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNISDRGTANYSQPYESPGLQL 420

Qy         447 KDSETELPPETTERPNYESYSHRLSHIGLISQSRVHVPVYSWTHRSADRTNTISSDSITQ 506
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Db         421 KDSETELPPETTERPNYESYSHRLSHIGIILQSRVNVPVYSWTHRSADRTNTIGPNRITQ 480

Qy         507 IPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ 566
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Db         481 IPMVKASELPQGTTVVRGPGFTGGDILRRTNTGGFGPIRVTVNGPLTQRYRIGFRYASTV 540

Qy         567 TMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFRFAEFPVGISASGSQ-TAGISISNNAG 625
                    |: ||:|  :  |  ||:: : |   :|    |    : :  |     ||   :|
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Qy         626 RQTFHFDKIEFIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 685
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Db         601 NGEVYIDKIEIIPVTATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 660

Qy         686 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 745
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 720

Qy         746 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 805
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Db         721 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 780

Qy         806 EDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 865
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Qy        866 RDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 925
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Db        841 RDGEKCAHHSHHFSLDIDVGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 900

Qy        926 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKL 985
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Db        901 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHAADKL 960

Qy        986 VHRIREAYLSELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGH 1045
                 |||||||||||| |||||||||||||| |||||||||||||||||||||||| |||||||
Db        961 VHRIREAYLSELPVIPGVNAEIFEELEGHIITAISLYDARNVVKNGDFNNGLTCWNVKGH 1020

Qy       1046 VDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDE 1105
                 ||||||||| |||||||||||||||| |||||||||||||||||||||||||||||||
Db       1021 VDVQQSHHRSDLVIPEWEAEVSQAVRVCPGCGYILRVTAYKEGYGEGCVTIHEIENNTDE 1080

Qy       1106 LKFKNCEEEEVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAYEVDTTASVNYKPTY 1161
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Db       1081 LKFKNREEEEVYPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVNYKPTY 1140

Qy       1162 EEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSV 1221
                 ||||||||||||||||||||||:|||||:|||||||||| ||||||||||||||||||||
Db       1141 EEETYTDVRRDNHCEYDRGYVNYPPVPAGYVTKELEYFPETDTVWIEIGETEGKFIVDSV 1200

Qy       1222 ELLLMEE 1228
                 |||||||
Db       1201 ELLLMEE 1207
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RESULT 7
US-08-459-595A-7
; Sequence 7, Application US/08459595A
; Patent No. 6018104
;  GENERAL INFORMATION:
;    APPLICANT:  Koziel, Michael G.
;    APPLICANT:  Desai, Nalini M.
;    APPLICANT:  Lewis, Kelly S.
;    APPLICANT:  Kramer, Vance C.
;    APPLICANT:  Warren, Gregory W.
;    APPLICANT:  Evola, Stephen V.
;    APPLICANT:  Crossland, Lyle D.
;    APPLICANT:  Wright, Martha S.
;    APPLICANT:  Merlin, Ellis J.
;    APPLICANT:  Launis, Karen L.
;    APPLICANT:  Rothstein, Steven J.
;    APPLICANT:  Bowman, Cindy G.
;    APPLICANT:  Dawson, John L.
;    APPLICANT:  Dunder, Erik M.
;    APPLICANT:  Pace, Gary M.
;    APPLICANT:  Suttie, Janet L.
;    TITLE OF INVENTION:  SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;    TITLE OF INVENTION:  INSECTICIDAL ACTIVITY IN MAIZE
;    NUMBER OF SEQUENCES:  94
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6018104artis Corporation
;      STREET:  Patent & Trademark Dept., 520 White Plains
;      STREET:  Rd., POB 2005
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10591-9005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,595A
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,715
;      FILING DATE:  25-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/772,027
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pace, Gary M.
;      REGISTRATION NUMBER:  40403
;      REFERENCE/DOCKET NUMBER:  CGC 1577/CIP/DIV3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)541-8582
;      TELEFAX:  (919)541-8689
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1207 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-459-595A-7

  Query Match             87.4%;  Score 5659.5;  DB 3;  Length 1207;
  Best Local Similarity   89.4%;  Pred. No. 0;
  Matches 1079;  Conservative   34;  Mismatches   89;  Indels    5;  Gaps    2;

Qy          27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRILGVLGVPFAGQIASFYSFLV 86
                 ||| |||||||||||||||:| ||||||||||||||||||||||:||||||||
Db           1 MDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLV 60

Qy          87 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 146
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 120

Qy         147 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 206
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 180

Qy         207 GLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 266
                 ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db         181 GLTSQEIQRYYERQVERTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 240

Qy         267 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIETAVIRS 326
                 |||||||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db         241 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIEAAAIRS 300

Qy         327 PHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPIGGGLNTSTHGSTNTSINPVRLS 386
                 |||||||||||||| ||||| |||||||||||||||||||||||:||||||||| |
Db         301 PHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLR 360

Qy         387 FFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFNFRNPQNTFERGTANYSQPYESPGLQL 446
                 | ||||| |||||||||||||||||||||||||||| ||||  :||||||||||||||||
Db         361 FASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNISDRGTANYSQPYESPGLQL 420

Qy         447 KDSETELPPETTERPNYESYSHRLSHIGLISQSRVHVPVYSWTHRSADRTNTISSDSITQ 506
                 |||||||||||||||||||||||||:| ||||:|||||||||||||||  : |||
Db         421 KDSETELPPETTERPNYESYSHRLSHIGIILQSRVNVPVYSWTHRSADRTNTIGPNRITQ 480

Qy         507 IPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ 566
                 ||:||:  |  ||:|| |||||||||:|    |    : :  |    ||||:  |||::
Db         481 IPMVKASELPQGTTVVRGPGFTGGDILRRTNTGGFGPIRVTVNGPLTQRYRIGFRYASTV 540

Qy         567 TMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFRFAEFPVGISASGSQ-TAGISISNNAG 625
                     |: ||:|  :  |  ||:: : |   :|    |    : :  |      ||   :|
Db         541 DFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTTPFTFTQIQDIIRTSIQGLSG 600

Qy         626 RQTFHFDKIEFIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 685
                     : |||| ||:|||||||||||||||||||||||||||||||||||||||||||||
Db         601 NGEVYIDKIEIIPVTATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 660

Qy         686 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 745
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 720
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Qy        746 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 780

Qy        806 EDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 865
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db        781 EDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 840

Qy        866 RDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 925
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        841 RDGEKCAHHSHHFSLDIDVGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 900

Qy        926 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKL 985
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        901 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHAADKL 960

Qy        986 VHRIREAYLSELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGH 1045
              |||||||||||| |||||||||||||||| |||||||||||||||||||||| |||||||
Db        961 VHRIREAYLSELPVIPGVNAEIFEELEGHIITAISLYDARNVVKNGDFNNGLTCWNVKGH 1020

Qy       1046 VDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDE 1105
              |||||||||| |||||||||||||||||| |||||||||||||||||||||||||||||||
Db       1021 VDVQQSHHRSDLVIPEWEAEVSQAVRVCPGCGYILRVTAYKEGYGEGCVTIHEIENNTDE 1080

Qy       1106 LKFKNCEEEEVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAYEVDTTASVNYKPTY 1161
              ||||| |||||||||||||||||||||     |||||||||||||||||||||||||||||
Db       1081 LKFKNREEEEVYPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVNYKPTY 1140

Qy       1162 EEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSV 1221
              |||||||||||||||||||||||:||||:|||||||||| ||||||||||||||||||||
Db       1141 EEETYTDVRRDNHCEYDRGYVNYPPVPAGYVTKELEYFPETDTVWIEIGETEGKFIVDSV 1200

Qy       1222 ELLLMEE 1228
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Db       1201 ELLLMEE 1207
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RESULT 8
US-08-459-504B-7
; Sequence 7, Application US/08459504B
; Patent No. 6075185
;  GENERAL INFORMATION:
;    APPLICANT:  Koziel, Michael G.
;    APPLICANT:  Desai, Nalini M.
;    APPLICANT:  Lewis, Kelly S.
;    APPLICANT:  Kramer, Vance C.
;    APPLICANT:  Warren, Gregory W.
;    APPLICANT:  Evola, Stephen V.
;    APPLICANT:  Crossland, Lyle D.
;    APPLICANT:  Wright, Martha S.
;    APPLICANT:  Merlin, Ellis J.
;    APPLICANT:  Launis, Karen L.
;    APPLICANT:  Rothstein, Steven J.
;    APPLICANT:  Bowman, Cindy G.
;    APPLICANT:  Dawson, John L.
;    APPLICANT:  Dunder, Erik M.
;    APPLICANT:  Pace, Gary M.
;    APPLICANT:  Suttie, Janet L.
;    TITLE OF INVENTION:  SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;    TITLE OF INVENTION:  INSECTICIDAL ACTIVITY IN MAIZE
;    NUMBER OF SEQUENCES:  94
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6075185artis Corporation
;      STREET:  3054 Cornwallis Road
;      CITY:  Research Triangle Park
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,504B
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/459,595
;      FILING DATE:  02-JUN-1995
;      APPLICATION NUMBER:  US 07/951,715
;      FILING DATE:  25-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/772,027
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meigs, J. Timothy
;      REGISTRATION NUMBER:  38,241
;      REFERENCE/DOCKET NUMBER:  CGC1577/CIP/DIV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)541-8587
;      TELEFAX:  (919)541-8689
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1207 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-459-504B-7

  Query Match             87.4%;  Score 5659.5;  DB 3;  Length 1207;
  Best Local Similarity   89.4%;  Pred. No. 0;
  Matches 1079;  Conservative   34;  Mismatches   89;  Indels    5;  Gaps    2;

Qy         27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRILGVLGVPFAGQIASFYSFLV 86
              ||| |||||||||||||||:| |||||||||||||||||||||||:||||||||
Db          1 MDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLV 60

Qy         87 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 120

Qy        147 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 180

Qy        207 GLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 266
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLTSQEIQRYYERQVERTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 240

Qy        267 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIETAVIRS 326
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        241 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIEAAAIRS 300

Qy        327 PHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPIGGGLNTSTHGSTNTSINPVRLS 386
              |||||||||||||| ||||| ||||||||||||||||||||||:|||||||| |
Db        301 PHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLR 360

Qy        387 FFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFNFRNPQNTFERGTANYSQPYESPGLQL 446
              | ||||| |||||||||||||||||||||||||| ||||  :|||||||||||||||||
Db        361 FASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNISDRGTANYSQPYESPGLQL 420

Qy        447 KDSETELPPETTERPNYESYSHRLSHIGLISQSRVHVPVYSWTHRSADRTNTISSDSITQ 506
              |||||||||||||||||||||||||||||:| ||||:|||||||||||||||  : |||
Db        421 KDSETELPPETTERPNYESYSHRLSHIGIILQSRVNVPVYSWTHRSADRTNTIGPNRITQ 480

Qy        507 IPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ 566
              ||:||:  |  ||:|| |||||||||:|    |    : :  |    ||||:  |||::
Db        481 IPMVKASELPQGTTVVRGPGFTGGDILRRTNTGGFGPIRVTVNGPLTQRYRIGFRYASTV 540

Qy        567 TMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFRFAEFPVGISASGSQ-TAGISISNNAG 625
                  |: ||:|  :  |  ||:: : |   :|    |    : :  |     ||   :|
Db        541 DFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTTPFTFTQIQDIIRTSIQGLSG 600

Qy        626 RQTFHFDKIEFIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 685
                  : |||| ||:||||||||||||||||||||||||||||||||||||||||||||||
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Db        601 NGEVYIDKIEIIPVTATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 660

Qy        686 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 720

Qy        746 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 780

Qy        806 EDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 865
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db        781 EDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 840

Qy        866 RDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 925
              ||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDGEKCAHHSHHFSLDIDVGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 900

Qy        926 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKL 985
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        901 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHAADKL 960

Qy        986 VHRIREAYLSELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGH 1045
              |||||||||||| |||||||||||||| |||||||||||||||||||| |||||||||||
Db        961 VHRIREAYLSELPVIPGVNAEIFEELEGHIITAISLYDARNVVKNGDFNNGLTCWNVKGH 1020

Qy       1046 VDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDE 1105
              |||||||||| |||||||||||||||| |||||||||||||||||||||||||||||||||
Db       1021 VDVQQSHHRSDLVIPEWEAEVSQAVRVCPGCGYILRVTAYKEGYGEGCVTIHEIENNTDE 1080

Qy       1106 LKFKNCEEEEVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAYEVDTTASVNYKPTY 1161
              ||||| |||||||||||||||||||||     |||||||||||||||||||||||||||||
Db       1081 LKFKNREEEEVYPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVNYKPTY 1140

Qy       1162 EEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSV 1221
              ||||||||||||||||||||||||||:||||:|||||||||||| ||||||||||||||||
Db       1141 EEETYTDVRRDNHCEYDRGYVNYPPVPAGYVTKELEYFPETDTVWIEIGETEGKFIVDSV 1200

Qy       1222 ELLLMEE 1228
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Db       1201 ELLLMEE 1207


RESULT 9
US-08-459-444-7
; Sequence 7, Application US/08459444A
; Patent No. 6121014
;   GENERAL INFORMATION:
;        APPLICANT: Koziel, Michael G.
;                   Desai, Nalini M.
;                   Lewis, Kelly S.
;                   Kramer, Vance C.
;                   Warren, Gregory W.
;                   Evola, Stephen V.
;                   Crossland, Lyle D.
;                   Wright, Martha S.
;                   Merlin, Ellis J.
;                   Launis, Karen L.
;        TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
;                            NUCLEIC ACID CODING SEQUENCE
;        NUMBER OF SEQUENCES: 94
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
;             STREET: 3054 Cornwallis Road
;             CITY: Research Triangle Park
;             STATE: NC
;             COUNTRY: USA
;             ZIP: 27709
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/459,444A
;             FILING DATE: 02-Jun-1995
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 07/951,715
;             FILING DATE: 25-SEP-1992
;             APPLICATION NUMBER: US 07/772,027
;             FILING DATE: 04-OCT-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Meigs, J. Timothy
;             REGISTRATION NUMBER: 38,241
;             REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (919)541-8587
;             TELEFAX: (919)541-8689
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1207 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-459-444-7

  Query Match             87.4%;  Score 5659.5;  DB 3;  Length 1207;
  Best Local Similarity   89.4%;  Pred. No. 0;
  Matches 1079;  Conservative   34;  Mismatches   89;  Indels    5;  Gaps    2;

Qy         27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRILGVLGVPFAGQIASFYSFLV 86
              ||| |||||||||||||||:| ||||||||||||||||||||||:||||||||
Db          1 MDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLV 60

Qy         87 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 146
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Db         61 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 120

Qy        147 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 180

Qy        207 GLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 266
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLTSQEIQRYYERQVERTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 240

Qy        267 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIETAVIRS 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        241 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIEAAAIRS 300

Qy        327 PHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPIGGGLNTSTHGSTNTSINPVRLS 386
              |||||||||||||| ||||| ||||||||||||||||||||:|||||||| |
Db        301 PHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLR 360

Qy        387 FFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFNFRNPQNTFERGTANYSQPYESPGLQL 446
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Db        361 FASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNISDRGTANYSQPYESPGLQL 420

Qy        447 KDSETELPPETTERPNYESYSHRLSHIGLISQSRVHVPVYSWTHRSADRTNTISSDSITQ 506
              |||||||||||||||||||||||||||:| ||||:|||||||||||||  : |||
Db        421 KDSETELPPETTERPNYESYSHRLSHIGIILQSRVNVPVYSWTHRSADRTNTIGPNRITQ 480

Qy        507 IPLVKSFNLNSGTSVVSGPGPTGGDIIRTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ 566
              ||:||:  |  ||:|| |||||||||:|    |    : :  |    ||||:  |||::
Db        481 IPMVKASELPQGTTVVRGPGFTGGDILRRTNTGGFGPIRVTVNGPLTQRYRIGFRYASTV 540

Qy        567 TMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFRFAEFPVGISASGSQ-TAGISISNNAG 625
                       |: ||:|  :  |  ||:: : |   :|    |   : :  |    ||  :|
Db        541 DFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTTPFTFTQIQDIIRTSIQGLSG 600

Qy        626 RQTFHFDKIEFIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 685
                  : |||| ||:||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NGEVYIDKIEIIPVTATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 660
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Qy        686 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 720

Qy        746 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 780

Qy        806 EDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 865
              |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db        781 EDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 840

Qy        866 RDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 925
              ||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDGEKCAHHSHHFSLDIDVGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 900

Qy        926 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKL 985
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        901 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHAADKL 960

Qy        986 VHRIREAYLSELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGH 1045
              |||||||||||| |||||||||||||| |||||||||||||||||||||||| |||||||
Db        961 VHRIREAYLSELPVIPGVNAEIFEELEGHIITAISLYDARNVVKNGDFNNGLTCWNVKGH 1020

Qy       1046 VDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDE 1105
              |||||||||| |||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1021 VDVQQSHHRSDLVIPEWEAEVSQAVRVCPGCGYILRVTAYKEGYGEGCVTIHEIENNTDE 1080

Qy       1106 LKFKNCEEEEVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAYEVDTTASVNYKPTY 1161
              ||||| |||||||||||||||||||||     ||||||||||||||||||||||||||||
Db       1081 LKFKNREEEEVYPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVNYKPTY 1140

Qy       1162 EEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSV 1221
              ||||||||||||||||||||||:||||:|||||||||| ||||||||||||||||||||||
Db       1141 EEETYTDVRRDNHCEYDRGYVNYPPVPAGYVTKELEYFPETDTVWIEIGETEGKFIVDSV 1200

Qy       1222 ELLLMEE 1228
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Db       1201 ELLLMEE 1207


RESULT 10
US-09-053-549-8
; Sequence 8, Application US/09053549
; Patent No. 6121521
;  GENERAL INFORMATION:
;    APPLICANT:  Desai, Nalini
;    TITLE OF INVENTION:  No. 6121521el Insecticidal Protein and Gene
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6121521artis Corporation
;      STREET:  3054 Cornwallis Rd.
;      CITY:  Research Triangle Park
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/053,549
;      FILING DATE:  01-APR-1998
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pace, Gary M.
;      REGISTRATION NUMBER:  40,403
;      REFERENCE/DOCKET NUMBER:  CGC 1995
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-541-8582
;      TELEFAX:  919-541-8689
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1207 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-053-549-8

  Query Match             87.4%;  Score 5659.5;  DB 3;  Length 1207;
  Best Local Similarity   89.4%;  Pred. No. 0;
  Matches 1079;  Conservative   34;  Mismatches   89;  Indels    5;  Gaps    2;

Qy         27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRILGVLGVPFAGQIASFYSFLV 86
              ||| |||||||||||||||||:| |||||||||||||||||||||||||||:||||||||
Db          1 MDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLV 60

Qy         87 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 120

Qy        147 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 180

Qy        207 GLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 266
              |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLTSQEIQRYYERQVERTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 240

Qy        267 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIETAVIRS 326
              |||||||||||||||||||||||||||||||||||||||||||||||||||| | |||||
Db        241 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIEAAAIRS 300

Qy        327 PHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPIGGGLNTSTHGSTNTSINPVRLS 386
              ||||||||||||| ||||| |||||||||||||||||||||:|||||||| |
Db        301 PHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLR 360

Qy        387 FFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFNFRNPQNTFERGTANYSQPYESPGLQL 446
              | ||||| |||||||||||||||||||||||||| ||||  :|||||||||||||||||
Db        361 FASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNISDRGTANYSQPYESPGLQL 420

Qy        447 KDSETELPPETTERPNYESYSHRLSHIGLISQSRVHVPVYSWTHRSADRTNTISSDSITQ 506
              |||||||||||||||||||||||:| ||||:|||||||||||||||  : |||
Db        421 KDSETELPPETTERPNYESYSHRLSHIGIILQSRVNVPVYSWTHRSADRTNTIGPNRITQ 480

Qy        507 IPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ 566
              ||:||:  |  ||:|| |||||||||:|    |    : :  |    ||||:  |||::
Db        481 IPMVKASELPQGTTVVRGPGFTGGDILRRTNTGGFGPIRVTVNGPLTQRYRIGFRYASTV 540

Qy        567 TMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFRFAEFPVGISASGSQ-TAGISISNNAG 625
                    |: ||:|  :  |  ||:: : |   :|    |    : :  |     ||   :|
Db        541 DFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTTPFTFTQIQDIIRTSIQGLSG 600

Qy        626 RQTFHFDKIEFIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 685
                  : |||| ||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NGEVYIDKIEIIPVTATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 660

Qy        686 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 720

Qy        746 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 780

Qy        806 EDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 865
              |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db        781 EDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 840

Qy        866 RDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 925
              ||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDGEKCAHHSHHFSLDIDVGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 900

Qy        926 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKL 985
              |||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
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Db        901 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHAADKL 960

Qy        986 VHRIREAYLSELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGH 1045
              |||||||||||| |||||||||||| |||||||||||||||||||||| |||||||
Db        961 VHRIREAYLSELPVIPGVNAEIFEELEGHIITAISLYDARNVVKNGDFNNGLTCWNVKGH 1020

Qy       1046 VDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDE 1105
              |||||||||| |||||||||||||||||| |||||||||||||||||||||||||||||
Db       1021 VDVQQSHHRSDLVIPEWEAEVSQAVRVCPGCGYILRVTAYKEGYGEGCVTIHEIENNTDE 1080

Qy       1106 LKFKNCEEEEVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAYEVDTTASVNYKPTY 1161
              ||||| |||||||||||||||||||||     |||||||||||||||||||||||||||
Db       1081 LKFKNREEEEVYPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVNYKPTY 1140

Qy       1162 EEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSV 1221
              ||||||||||||||||||||||||:||||:|||||||||| ||||||||||||||||||
Db       1141 EEETYTDVRRDNHCEYDRGYVNYPPVPAGYVTKELEYFPETDTVWIEIGETEGKFIVDSV 1200

Qy       1222 ELLLMEE 1228
              |||||||
Db       1201 ELLLMEE 1207


RESULT 11
US-09-547-422-7
; Sequence 7, Application US/09547422
; Patent No. 6320100
;  GENERAL INFORMATION:
;       APPLICANT: Koziel, Michael G.
;                  Desai, Nalini M.
;                  Lewis, Kelly S.
;                  Kramer, Vance C.
;                  Warren, Gregory W.
;                  Evola, Stephen V.
;                  Crossland, Lyle D.
;                  Wright, Martha S.
;                  Merlin, Ellis J.
;                  Launis, Karen L.
;       TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;                           INSECTICIDAL ACTIVITY IN MAIZE
;       NUMBER OF SEQUENCES: 94
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
;            STREET: 3054 Cornwallis Road
;            CITY: Research Triangle Park
;            STATE: NC
;            COUNTRY: USA
;            ZIP: 27709
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/547,422
;            FILING DATE: 11-Apr-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/459,595
;            FILING DATE: 02-JUN-1995
;            APPLICATION NUMBER: US 07/951,715
;            FILING DATE: 25-SEP-1992
;            APPLICATION NUMBER: US 07/772,027
;            FILING DATE: 04-OCT-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Meigs, J. Timothy
;            REGISTRATION NUMBER: 38,241
;            REFERENCE/DOCKET NUMBER: S-18805H
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (919)541-8587
;            TELEFAX: (919)541-8689
;  INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1207 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-547-422-7

  Query Match             87.4%;  Score 5659.5;  DB 3;  Length 1207;
  Best Local Similarity   89.4%;  Pred. No. 0;
  Matches 1079;  Conservative   34;  Mismatches   89;  Indels    5;  Gaps    2;

Qy         27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRILGVLGVPFAGQIASFYSFLV 86
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Db          1 MDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLV 60

Qy         87 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 120

Qy        147 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 206
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 180

Qy        207 GLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 266
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLTSQEIQRYYERQVERTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 240

Qy        267 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIETAVIRS 326
              |||||||||||||||||||||||||||||||||||||||||||||||||||| | |||||
Db        241 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIEAAAIRS 300

Qy        327 PHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPIGGGLNTSTHGSTNTSINPVRLS 386
              |||||||||||||| ||||| ||||||||||||||||||||:|||||||| |
Db        301 PHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLR 360

Qy        387 FFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFNFRNPQNTFERGTANYSQPYESPGLQL 446
              | ||||| |||||||||||||||||||||||| ||||  :||||||||||||||||||
Db        361 FASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNISDRGTANYSQPYESPGLQL 420

Qy        447 KDSETELPPETTERPNYESYSHRLSHIGLISQSRVHVPVYSWTHRSADRTNTISSDSITQ 506
              |||||||||||||||||||||||||||:| ||||:|||||||||||||  : |||
Db        421 KDSETELPPETTERPNYESYSHRLSHIGIILQSRVNVPVYSWTHRSADRTNTIGPNRITQ 480

Qy        507 IPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ 566
              ||:||:  |  ||:|| |||||||||:|    |   : :  |    ||||:  |||::
Db        481 IPMVKASELPQGTTVVRGPGFTGGDILRRTNTGGFGPIRVTVNGPLTQRYRIGFRYASTV 540

Qy        567 TMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFRFAEFPVGISASGSQ-TAGISISNNAG 625
                  |: ||:|  :  |  ||:: : |   :|    |    : :  |    ||   :|
Db        541 DFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTTPFTFTQIQDIIRTSIQGLSG 600

Qy        626 RQTFHFDKIEFIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 685
                 : |||| ||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NGEVYIDKIEIIPVTATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 660

Qy        686 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 745
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 720

Qy        746 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 805
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 780

Qy        806 EDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 865
              |||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db        781 EDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 840

Qy        866 RDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 925
              |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDGEKCAHHSHHFSLDIDVGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 900

Qy        926 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKL 985
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Db        901 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHAADKL 960

Qy        986 VHRIREAYLSELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGH 1045
              |||||||||||| |||||||||||||| |||||||||||||||||||||||| |||||||
Db        961 VHRIREAYLSELPVIPGVNAEIFEELEGHIITAISLYDARNVVKNGDFNNGLTCWNVKGH 1020

Qy       1046 VDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDE 1105
              |||||||||| |||||||||||||||||| |||||||||||||||||||||||||||||||
Db       1021 VDVQQSHHRSDLVIPEWEAEVSQAVRVCPGCGYILRVTAYKEGYGEGCVTIHEIENNTDE 1080

Qy       1106 LKFKNCEEEEVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAYEVDTTASVNYKPTY 1161
              ||||| |||||||||||||||||||||     |||||||||||||||||||||||||||||
Db       1081 LKFKNREEEEVYPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVNYKPTY 1140

Qy       1162 EEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSV 1221
              |||||||||||||||||||||||:|||||:|||||||||| ||||||||||||||||||||
Db       1141 EEETYTDVRRDNHCEYDRGYVNYPPVPAGYVTKELEYFPETDTVWIEIGETEGKFIVDSV 1200

Qy       1222 ELLLMEE 1228
              |||||||
Db       1201 ELLLMEE 1207


RESULT 12
US-09-988-462-7
; Sequence 7, Application US/09988462
; Patent No. 6720488
;   GENERAL INFORMATION:
;        APPLICANT: Koziel, Michael G.
;                   Desai, Nalini M.
;                   Lewis, Kelly S.
;                   Kramer, Vance C.
;                   Warren, Gregory W.
;                   Evola, Stephen V.
;                   Crossland, Lyle D.
;                   Wright, Martha S.
;                   Merlin, Ellis J.
;                   Launis, Karen L.
;        TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;                            INSECTICIDAL ACTIVITY IN MAIZE
;        NUMBER OF SEQUENCES: 94
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Syngenta Biotechnology, Inc.
;             STREET: 3054 Cornwallis Road
;             CITY: Research Triangle Park
;             STATE: NC
;             COUNTRY: USA
;             ZIP: 27709
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/988,462
;             FILING DATE: 20-No. 6720488-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 09/547,422
;             FILING DATE: 11-APR-2000
;             APPLICATION NUMBER: US 08/459,504
;             FILING DATE: 02-JUN-1995
;             APPLICATION NUMBER: US 07/951,715
;             FILING DATE: 25-SEP-1992
;             APPLICATION NUMBER: US 07/772,027
;             FILING DATE: 04-OCT-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Meigs, J. Timothy
;             REGISTRATION NUMBER: 38,241
;             REFERENCE/DOCKET NUMBER: S-18805I
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (919)541-8587
;             TELEFAX: (919)541-8689

;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1207 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-988-462-7

  Query Match            87.4%;  Score 5659.5;  DB 4;  Length 1207;
  Best Local Similarity  89.4%;  Pred. No. 0;
  Matches 1079;  Conservative   34;  Mismatches   89;  Indels    5;  Gaps    2;

Qy         27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRILGVLGVPFAGQIASFYSFLV 86
              ||| |||||||||||||||:| |||||||||||||||||||||||:||||||||
Db          1 MDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLV 60

Qy         87 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 120

Qy        147 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 180

Qy        207 GLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 266
              ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLTSQEIQRYYERQVERTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 240

Qy        267 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIETAVIRS 326
              |||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        241 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIEAAAIRS 300

Qy        327 PHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPIGGGLNTSTHGSTNTSINPVRLS 386
              |||||||||||||| ||||| |||||||||||||||||||||:|||||||| |
Db        301 PHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLR 360

Qy        387 FFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFNFRNPQNTFERGTANYSQPYESPGLQL 446
              | ||||| |||||||||||||||||||||||||| ||||  :|||||||||||||||||
Db        361 FASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNISDRGTANYSQPYESPGLQL 420

Qy        447 KDSETELPPETTERPNYESYSHRLSHIGLISQSRVHVPVYSWTHRSADRTNTISSDSITQ 506
              |||||||||||||||||||||||||||||:| ||||:|||||||||||||||  : |||
Db        421 KDSETELPPETTERPNYESYSHRLSHIGIILQSRVNVPVYSWTHRSADRTNTIGPNRITQ 480

Qy        507 IPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ 566
              ||:||:  |  ||:|| |||||||||:|    |   : :  |   ||||:  |||::
Db        481 IPMVKASELPQGTTVVRGPGFTGGDILRRTNTGGFGPIRVTVNGPLTQRYRIGFRYASTV 540

Qy        567 TMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFRFAEFPVGISASGSQ-TAGISISNNAG 625
                  |: ||:|  :  |  ||:: : |   :|    |    : :  |    ||   :|
Db        541 DFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTTPFTFTQIQDIIRTSIQGLSG 600

Qy        626 RQTFHFDKIEFIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 685
                 : |||| ||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NGEVYIDKIEIIPVTATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 660

Qy        686 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 720

Qy        746 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 780

Qy        806 EDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 865
              |||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db        781 EDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 840

Qy        866 RDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 925
              |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db        841 RDGEKCAHHSHHFSLDIDVGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 900
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Qy        926 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKL 985
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        901 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHAADKL 960

Qy        986 VHRIREAYLSELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGH 1045
              |||||||||||| |||||||||||||| |||||||||||||||||||| |||||||
Db        961 VHRIREAYLSELPVIPGVNAEIFEELEGHIITAISLYDARNVVKNGDFNNGLTCWNVKGH 1020

Qy       1046 VDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDE 1105
              |||||||||| |||||||||||||||| |||||||||||||||||||||||||||||||
Db       1021 VDVQQSHHRSDLVIPEWEAEVSQAVRVCPGCGYILRVTAYKEGYGEGCVTIHEIENNTDE 1080

Qy       1106 LKFKNCEEEEVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAYEVDTTASVNYKPTY 1161
              ||||| |||||||||||||||||||||      |||||||||||||||||||||||||||||
Db       1081 LKFKNREEEEVYPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVNYKPTY 1140

Qy       1162 EEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSV 1221
              |||||||||||||||||||||||:||||:|||||||||| ||||||||||||||||||||
Db       1141 EEETYTDVRRDNHCEYDRGYVNYPPVPAGYVTKELEYFPETDTVWIEIGETEGKFIVDSV 1200

Qy       1222 ELLLMEE 1228
              |||||||
Db       1201 ELLLMEE 1207
```

RESULT 13
US-09-053-549-2
; Sequence 2, Application US/09053549
; Patent No. 6121521
; GENERAL INFORMATION:
; APPLICANT: Desai, Nalini
; TITLE OF INVENTION: No. 6121521el Insecticidal Protein and Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121521artis Corporation
; STREET: 3054 Cornwallis Rd.
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,549
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-053-549-2

Query Match 83.9%; Score 5436.5; DB 3; Length 1227;
Best Local Similarity 84.3%; Pred. No. 0;
Matches 1040; Conservative 63; Mismatches 118; Indels 13; Gaps 5;

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Qy          1 LTSNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
              :|||||||||||     |||||| |||| |||||||||||||||:| ||||||||||
Db          1 MTSNRKNENEIIN-----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGI 55

Qy         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 120
                |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db         56 NIAGRILGVLGVPFAGQLASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 115

Qy        121 LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 175

Qy        181 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLN 240
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        176 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVERTRDYSDYCVEWYNTGLN 235

Qy        241 SLRGTNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 SLRGTNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG 295

Qy        301 VNMASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQ 360
              |||||||||||||||||| | |||||||||||||||| ||||| ||||||||||||||
Db        296 VNMASMNWYNNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQ 355

Qy        361 SRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFN 420
              ||||||||||||||:|||:|||| | | ||||| ||||||||||||||||||||||||||
Db        356 SRPIGGGLNTSTHGATNTTINPVTLRFASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFN 415

Qy        421 FRNPQNTFERGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLISQSR 480
              | ||||  :|||||||||||||||||||||||||||||||||||||||||||||||:| |||
Db        416 FTNPQNISDRGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGIILQSR 475

Qy        481 VHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGS 540
              |:|||||||||||||||  : |||||:||:  |  ||:|| |||||||||:|    |
Db        476 VNVPVYSWTHRSADRTNTIGPNRITQIPMVKASELPQGTTVVRGPGFTGGDILRRTNTGG 535

Qy        541 VLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFR 600
                 : :  |    ||||:  |||::      |: ||:|  :  |  ||:: : |   :|
Db        536 FGPIRVTVNGPLTQRYRIGFRYASTVDFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFV 595

Qy        601 FAEFPVGISASGSQT-AGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNAL 659
                  |   : :  |     ||   :|    : |||| ||:||||||||||||||||||
Db        596 RRAFTTPFTFTQIQNIIRTSIQGLSGNGEVYIDKIEIIPVTATFEAEYDLERAQEAVNAL 655

Qy        660 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDP 719
              |||||||||||||:|||||||||||||| |||||||||||||||||||||||||||||||
Db        656 FTNTNPRRLKTDVTNYHIDQVSNLVACLSDAFCLDEKRELLEKVKYAKRLSDERNLLQDP 715

Qy        720 NFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNEC 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 NFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNEC 775

Qy        780 YPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVE 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        776 YPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVE 835

Qy        840 SPIGRCGEPNRCAPHPEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVF 899
              |||||||||||||| ||||||||||||||||||||||||||:|||||:|:||||||:|
Db        836 SPIGRCGEPNRCAPHLEWNPDLDCSCRDGEKCAHHSHHFSLDIDVGCTDLNEDLGVWVIF 895

Qy        900 KIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVD 959
              |||||:|||||||||:|||||:||||:|||||||||||||||: ||  || ||||:||
Db        896 KIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVD 955

Qy        960 ALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITAI 1019
              ||||:|||:|||||||| ||||||| || |||||| |||||||||| |||||||| ||
Db        956 ALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAF 1015

Qy       1020 SLYDARNVVKNGDFNNGLACWNVKGHVDV-QQSHHRSVLVIPEWEAEVSQAVRVCPGRGY 1078
              ||||||||:|||||||:|||||||||| :|::|||||:|||||||| |||||||||
Db       1016 SLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNHRSVLVVPEWEAEVSQEVRVCPGRGY 1075

Qy       1079 ILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTA----HQGTA 1134
              |||||||||||||||||||||||||||||| || |||||| :| |||||||    ::||
Db       1076 ILRVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEVYPNNTVTCNDYTATQEEYEGT- 1134

Qy       1135 VCNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTK 1194
                 ||| ||: ||| ::: :|  |||: ||| |||| || :||| :| |||||:||
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Db       1135 -YTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESNRGYGDYTPLPAGYVTK 1193

Qy       1195 ELEYFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
              |||||||||||||||||| ||||||||||||
Db       1194 ELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1227


RESULT 14
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322687
;  GENERAL INFORMATION:
;    APPLICANT:  Donovan, William P.
;    APPLICANT:  Tan, Yuping
;    APPLICANT:  Jany, Christine S.
;    APPLICANT:  Gonzalez Jr., Jose M.
;    TITLE OF INVENTION:  BACILLUS THURINGIENSIS cryET4 AND cryET5
;    TITLE OF INVENTION:  TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Panitch Schwarze Jacobs & Nadel c/o A.S.
;      ADDRESSEE:  Nadel
;      STREET:  1601 Market Street, 36th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/100,709
;      FILING DATE:  19930729
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Egolf, Christopher
;      REGISTRATION NUMBER:  27633
;      REFERENCE/DOCKET NUMBER:  7205-49
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-757-1590
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1229 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-100-709-4

  Query Match             80.8%;  Score 5237.5;  DB 1;  Length 1229;
  Best Local Similarity   79.9%;  Pred. No. 0;
  Matches  983;  Conservative   94;  Mismatches  149;  Indels    5;  Gaps    3;

Qy          1 LTSNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
              |||||||||||||||||| ||| ||||:||||||||||||:|| |||:| ||||||||||
Db          1 LTSNRKNENEIINALSIPTVSNPSTQMNLSPDARIEDSLCVAEVNNIDPFVSASTVQTGI 60

Qy         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 120
              ||||||||||||||||:|||||||||||||| ||| |||||||||||| ||:||| ||||
Db         61 NIAGRILGVLGVPFAGQLASFYSFLVGELWPSGRDPWEIFLEHVEQLIRQQVTENTRNTA 120

Qy        121 LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 180
              :|||:|||  :|:|||:|| ||:||:|||:||::  :|:|||||   |:||| |||:|||
Db        121 IARLEGLGRGYRSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIRNEEVP 180

Qy        181 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLN 240
              ||||||||||||||||||||||:|: | :: :||: |:  | :||::||:|||||||
Db        181 LLMVYAQAANLHLLLLRDASLFGSEWGMASSDVNQYYQEQIRYTEEYSNHCVQWYNTGLN 240

Qy        241 SLRGTNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG 300
              :|||||| ||:|||||||||||||||||||||||||||||||||||||:||| || |
Db        241 NLRGTNAESWLRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGRTN 300

Qy        301 V--NMASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHT 358
                 || ||:||||||||||| |: | |||||| |||||:| |||||:|:|| || ||
Db        301 APSGFASTNWFNNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMNYWVGHR 360

Qy        359 IQSRPIGGGLNTSTHGST-NTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTV 417
              :  ||||| ||||| | | ||||||| | | ||||| ||| ||  :  ::  |::|||
Db        361 LNFRPIGGTLNTSTQGLTNNTSINPVTLQFTSRDVYRTESNAGTNI--LFTTPVNGVPWA 418

Qy        418 RFNFRNPQNTFERGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLIS 477
              |||| |||| :|||   |||||:  |:|| |||||||||||||||||||||||||||||
Db        419 RFNFINPQNIYERGATTYSQPYQGVGIQLFDSETELPPETTERPNYESYSHRLSHIGLII 478

Qy        478 QSRVHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNV 537
               : :  ||||||||||||||||  : ||||||||: ||:|| :|| |||||||||:|
Db        479 GNTLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGDILRRTN 538

Qy        538 NGSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQ 597
              |:   :  || |    ||||||:|||::  :     : |:|     |  ||:  ::|  :
Db        539 TGTFGDIRLNINVPLSQRYRVRIRYASTTDLQFFTRINGTTVNIGNFSRTMNRGDNLEYR 598

Qy        598 SFRFAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVN 657
              ||| | |    :  :|:     : :   |  : |::||:|   ||||||||||||:|||
Db        599 SFRTAGFSTPFNFLNAQSTFTLGAQSFSNQEVYIDRVEFVPAEVTFEAEYDLERAQKAVN 658

Qy        658 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQ 717
              ||||:|||||||||||||||||:|||||||||||||| ||||||||||||||||
Db        659 ALFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFEKVKYAKRLSDERNLLQ 718

Qy        718 DPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFN 777
              |||||:|  |  | : |||| ||:| |||||||| |:||||||||||||||||||||||
Db        719 DPNFTFISGQLSFASIDGQSNFPSINELSEHGWWGSANVTIQEGNDVFKENYVTLPGTFN 778

Qy        778 ECYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLS 837
              |||| ||||||||||||||||||||||||||||||||||||||||||||||:|:||||
Db        779 ECYPNYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTDSLWPLS 838

Qy        838 VESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWV 897
              ||||||||||||||||||||||||||||:||||||||:||||:||||||||||||
Db        839 VESPIGRCGEPNRCAPHFEWNPDLDCSCRDGERCAHHSHHFTLDIDVGCTDLHENLGVWV 898

Qy        898 VFKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEA 957
              |||||||||:|||||||||||:||||||||||||||||||||||||||||||||||||||
Db        899 VFKIKTQEGYARLGNLEFIEEKPLIGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEA 958

Qy        958 VDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIIT 1017
              |||||||||::|||||||||||||||||||||||||||| ||||||||||||| |||
Db        959 VDALFVDSQYDQLQADTNIGMIHAADKLVHRIREAYLSELPVIPGVNAEIFEELEGHIIT 1018

Qy       1018 AISLYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRG 1077
              |:|||||||||||||||| ||||||||||||||| |||||||||||||||||||||||
Db       1019 AMSLYDARNVVKNGDFNNGLTCWNVKGHVDVQQSHHRSDLVIPEWEAEVSQAVRVCPGRG 1078

Qy       1078 YILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAVCN 1137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1079 YILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAACN 1138

Qy       1138 SRNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELE 1197
              |||||||||||||||||||||||||||||||||||||||||||||||:||||:|||||
Db       1139 SRNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPVPAGYVTKELE 1198

Qy       1198 YFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
              |||||| ||||||||||||||||||||||||
Db       1199 YFPETDTVWIEIGETEGKFIVDSVELLLMEE 1229


RESULT 15
US-08-176-865-4
; Sequence 4, Application US/08176865
; Patent No. 5616319
;  GENERAL INFORMATION:
;    APPLICANT:  Donovan, William P.
;    APPLICANT:  Tan, Yuping
```

```
;    APPLICANT:  Jany, Christine S.
;    APPLICANT:  Gonzalez Jr., Jose M.
;    TITLE OF INVENTION:  BACILLUS THURINGIENSIS cryET4 AND cryET5
;    TITLE OF INVENTION:  TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Panitch Schwarze Jacobs & Nadel c/o A.S.
;      ADDRESSEE:  Nadel
;      STREET:  1601 Market Street, 36th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/176,865
;      FILING DATE:  30-DEC-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/100,709
;      FILING DATE:  29-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Egolf, Christopher
;      REGISTRATION NUMBER:  27633
;      REFERENCE/DOCKET NUMBER:  7205-49
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-757-1590
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1229 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-176-865-4

  Query Match             80.8%;  Score 5237.5;  DB 1;  Length 1229;
  Best Local Similarity   79.9%;  Pred. No. 0;
  Matches  983;  Conservative   94;  Mismatches  149;  Indels    5;  Gaps    3;

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Qy         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 120
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Db        181 LLMVYAQAANLHLLLLRDASLFGSEWGMASSDVNQYYQEQIRYTEEYSNHCVQWYNTGLN 240

Qy        241 SLRGTNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG 300
              :|||||| ||:|||||||||||||||||||||||||||||||||||:||| || |
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Qy        301 V--NMASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHT 358
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Db        301 APSGFASTNWFNNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMNYWVGHR 360

Qy        359 IQSRPIGGGLNTSTHGST-NTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTV 417
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Qy        418 RFNFRNPQNTFERGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLIS 477
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Qy        478 QSRVHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNV 537
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Db        479 GNTLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGDILRRTN 538

Qy        538 NGSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQ 597
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Db        839 VESPIGRCGEPNRCAPHFEWNPDLDCSCRDGERCAHHSHHFTLDIDVGCTDLHENLGVWV 898

Qy        898 VFKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEA 957
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Qy       1198 YFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
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Search completed: May 24, 2005, 14:13:54
Job time : 52 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 24, 2005, 14:10:21 ; Search time 164 Seconds
(without alignments)
2504.728 Million cell updates/sec

Title: US-10-614-524-2
Perfect score: 6479
Sequence: 1 LTSNRKNENEIINALSIPAV.....IGETEGKFIVDSVELLLMEE 1228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6479	100.0	1228	15	US-10-614-524-2	Sequence 2, Appli
2	6464	99.8	1228	15	US-10-428-961-38	Sequence 38, Appl
3	5912.5	91.3	1227	15	US-10-428-961-63	Sequence 63, Appl
4	5745	88.7	1228	17	US-10-926-819-8	Sequence 8, Appli
5	5742	88.6	1228	16	US-10-809-953-10	Sequence 10, Appl
6	5659.5	87.4	1207	10	US-09-988-462-7	Sequence 7, Appli
7	5108	78.8	1186	9	US-09-826-660-23	Sequence 23, Appl
8	3502.5	54.1	1189	10	US-09-972-175-59	Sequence 59, Appl
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11	3500.5	54.0	1189	14	US-10-200-522-2	Sequence 2, Appli
12	3496.5	54.0	1189	10	US-09-972-175-61	Sequence 61, Appl
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15	3495.5	54.0	1189	17	US-10-926-819-9	Sequence 9, Appli
16	3494.5	53.9	1189	10	US-09-972-175-4	Sequence 4, Appli
17	3494.5	53.9	1189	10	US-09-972-175-6	Sequence 6, Appli
18	3494.5	53.9	1189	14	US-10-200-522-4	Sequence 4, Appli
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20	3493.5	53.9	1189	10	US-09-972-175-12	Sequence 12, Appl
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22	3490.5	53.9	1189	10	US-09-972-175-8	Sequence 8, Appli
23	3490.5	53.9	1189	14	US-10-200-522-8	Sequence 8, Appli
24	3487.5	53.8	1189	10	US-09-972-175-10	Sequence 10, Appl
25	3487.5	53.8	1189	14	US-10-200-522-10	Sequence 10, Appl
26	3482.5	53.8	1189	16	US-10-809-953-8	Sequence 8, Appli
27	3479.5	53.7	1189	14	US-10-102-469-20	Sequence 20, Appl
28	3476.5	53.7	1189	11	US-09-837-961-6	Sequence 6, Appli
29	3476.5	53.7	1189	16	US-10-825-751-6	Sequence 6, Appli
30	3463	53.4	1181	10	US-09-988-462-11	Sequence 11, Appl
31	3463	53.4	1181	10	US-09-988-462-13	Sequence 13, Appl
32	3463	53.4	1181	10	US-09-988-462-17	Sequence 17, Appl
33	3463	53.4	1181	10	US-09-988-462-28	Sequence 28, Appl
34	3463	53.4	1181	15	US-10-136-998A-4	Sequence 4, Appli
35	3463	53.4	1181	15	US-10-136-998A-8	Sequence 8, Appli
36	3463	53.4	1181	15	US-10-136-998A-10	Sequence 10, Appl
37	3463	53.4	1181	15	US-10-136-998A-12	Sequence 12, Appl
38	3460	53.4	1193	9	US-09-873-873-30	Sequence 30, Appl
39	3460	53.4	1193	10	US-09-916-956A-30	Sequence 30, Appl
40	3460	53.4	1193	10	US-09-997-914-30	Sequence 30, Appl
41	3460	53.4	1193	14	US-10-365-645-30	Sequence 30, Appl
42	3460	53.4	1193	15	US-10-672-163-30	Sequence 30, Appl
43	3460	53.4	1193	16	US-10-739-482-30	Sequence 30, Appl
44	3460	53.4	1193	16	US-10-817-182-30	Sequence 30, Appl
45	3459	53.4	1177	9	US-09-873-873-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-614-524-2

Query Match 100.0%; Score 6479; DB 15; Length 1228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 38, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-38

Query Match 99.8%; Score 6464; DB 15; Length 1228;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1224; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db        361 SRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFN 420

Qy        421 FRNPQNTFERGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLISQSR 480

Db        421 FRNPQNTFERGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLISQSR 480

Qy        481 VHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGS 540

Db        481 VHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGS 540
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Qy        541 VLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFR 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFR 600

Qy        601 FAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNALF 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 FAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNALF 660

Qy        661 TNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPN 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPN 720

Qy        721 PTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNECY 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNECY 780

Qy        781 PTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVES 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 PTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVES 840

Qy        841 PIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFK 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 PIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFK 900

Qy        901 IKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 IKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDA 960

Qy        961 LFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITAIS 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 LFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITAIS 1020

Qy       1021 LYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYIL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 LYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYIL 1080

Qy       1081 RVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAVCNSRN 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db       1081 RVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAACNSRN 1140

Qy       1141 AGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEYFP 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db       1141 AGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYVTKELEYFP 1200

Qy       1201 ETDKVWIEIGETEGKFIVDSVELLLMEE 1228
              |||||||||||||| |||||:|||||||
Db       1201 ETDKVWIEIGETEGTFIVDSIELLLMEE 1228
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RESULT 3
US-10-428-961-63
; Sequence 63, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 1227
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-63

Query Match 91.3%; Score 5912.5; DB 15; Length 1227;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1127; Conservative 36; Mismatches 62; Indels 5; Gaps 3;

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Qy          1 LTSNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
              |||||||||||||||||||||||| ||:|| |||||||||||||||:| ||||||||||
Db          1 LTSNRKNENEIINALSIPAVSNHSAQMNLSTDARIEDSLCIAEGNNIDPFVSASTVQTGI 60

Qy         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 120
              |||||||||||||||||||||||||||||||||| ||||||||| || ||:||| |:||
Db         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDPWEIFLEHVEHLIRQQVTENTRDTA 120

Qy        121 LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 180
              ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LARLQGLGNSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 180

Qy        181 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLN 240
              |||||||||||||||||||||||||||||||||||||||||||||:||:|||||  |||||||
Db        181 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEKTREYSDYCARWYNTGLN 240

Qy        241 SLRGTNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG 300
              :|||||| ||:|||||||||||||||||||||||| ||:||||||||:||| || |
Db        241 NLRGTNAESWLRYNQFRRDLTLGVLDLVALFPSYDTRVYPMNTSAQLTREIYTDPIGRTN 300

Qy        301 V--NMASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHT 358
                   || ||:|||||||||| |||| |||||| ||||||| |||| |::| || ||
Db        301 APSGFASTNWFNNNAPSFSAIEAAVIRPPHLLDFPEQLTIFSVLSRWSNTQYMNYWVGHR 360

Qy        359 IQSRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTVR 418
              ::|| | | |:| |||:|||||||| | | ||||| |||:||: :  :   |::|||  |
Db        361 LESRTIRGSLSTWTHGNTNTSINPVTLQFTSRDVYRTESPAGINI--LLTTPVNGVPWAR 418

Qy        419 FNFRNPQNTFERGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLISQ 478
              ||:||| |:  ||:  |:  |    | || |||||||||||||||||||||:| |||
Db        419 FNWRNPLNSL-RGSLLYTIGYTGVGTQLFDSETELPPETTERPNYESYSHRLSNIRLISG 477

Qy        479 SRVHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVN 538
              : :  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 NTLRAPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVN 537

Qy        539 GSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQS 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 GSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQS 597

Qy        599 FRFAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNA 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 FRFAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNA 657

Qy        659 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 718
              |||||||||||| |||||||:||||||||||||||||||||||||||||||||||||||
Db        658 LFTNTNPRRLKTGVTDYHIDEVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 717

Qy        719 PNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNE 778
              |||||||||||| | ||||||||||||||||||||||||||||||||||||||||||||
Db        718 PNFTSINKQPDFNSNNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNE 777

Qy        779 CYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSV 838
              ||||||||||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        778 CYPTYLYQKIGEAELKAYTRYQLSGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSV 837

Qy        839 ESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVV 898
              |||||||||||||||||||||||||||||||||||||||||:|| ||||||||||||
Db        838 ESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDVGCIDLHENLGVWVV 897

Qy        899 FKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAV 958
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 FKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAV 957

Qy        959 DALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITA 1018
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Db        958 DALFVDSQYDRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITA 1017

Qy       1019 ISLYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGY 1078
Db       1018 ISLYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGY 1077

Qy       1079 ILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAVCNS 1138
Db       1078 ILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAVCNS 1137

Qy       1139 RNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEY 1198
Db       1138 RNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPVPAGYMTKELEY 1197

Qy       1199 FPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
Db       1198 FPETDKVWIEIGETEGKFIVDSVELLLMEE 1227
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RESULT 4
US-10-926-819-8
; Sequence 8, Application US/10926819
; Publication No. US20050049410A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-003, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/281577
; CURRENT APPLICATION NUMBER: US/10/926,819
; CURRENT FILING DATE: 2004-08-26
; PRIOR APPLICATION NUMBER: 60/498,518
; PRIOR FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis serovar entomocidus
US-10-926-819-8

Query Match 88.7%; Score 5745; DB 17; Length 1228;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1098; Conservative 35; Mismatches 90; Indels 10; Gaps 3;

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Qy          1 LTSNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db          1 MTSNRKNENEIIN-----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGI 55

Qy         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 120
Db         56 NIAGRILGVLGVPFAGQLASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 115

Qy        121 LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 180
Db        116 LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 175

Qy        181 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLN 240
Db        176 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVERTRDYSDYCVEWYNTGLN 235

Qy        241 SLRGTNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG 300
Db        236 SLRGTNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG 295

Qy        301 VNMASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQ 360
Db        296 VNMASMNWYNNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQ 355

Qy        361 SRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFN 420
Db        356 SRPIGGGLNTSTHGATNTSINPVTLRFASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFN 415

Qy        421 FRNPQNTFERGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLISQSR 480
Db        416 FTNPQNISDRGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGIILQSR 475

Qy        481 VHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGS 540
Db        476 VNVPVYSWTHRSADRTNTIGPNRITQIPMVKASELPQGTTVVRGPGFTGGDILRRTNTGG 535

Qy        541 VLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFR 600
Db        536 FGPIRVTVNGPLTQRYRIGFRYASTVDFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFV 595

Qy        601 FAEFPVGISASGSQ-TAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNAL 659
Db        596 RRAFTTPFTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFEAEYDLERAQEAVNAL 655

Qy        660 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDP 719
Db        656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDP 715

Qy        720 NFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNEC 779
Db        716 NFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNEC 775

Qy        780 YPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVE 839
Db        776 YPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVE 835

Qy        840 SPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVF 899
Db        836 SPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDVGCTDLHENLGVWVVF 895

Qy        900 KIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVD 959
Db        896 KIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVD 955

Qy        960 ALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITAI 1019
Db        956 ALFVDSQYDRLQADTNIGMIHAADKLVHRIREAYLSELPVIPGVNAEIFEELEGHIITAI 1015

Qy       1020 SLYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYI 1079
Db       1016 SLYDARNVVKNGDFNNGLTCWNVKGHVDVQQSHHRSDLVIPEWEAEVSQAVRVCPGCGYI 1075

Qy       1080 LRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTA----V 1135
Db       1076 LRVTAYKEGYGEGCVTIHEIENNTDELKFKNREEEEVYPTDTGTCNDYTAHQGTAGCADA 1135

Qy       1136 CNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKE 1195
Db       1136 CNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPVPAGYVTKE 1195

Qy       1196 LEYFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
Db       1196 LEYFPETDTVWIEIGETEGKFIVDSVELLLMEE 1228
```

RESULT 5
US-10-809-953-10
; Sequence 10, Application US/10809953
; Publication No. US20040181825A1
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTI
; TITLE OF INVENTION: CRYSTAL PROTEINS
; FILE REFERENCE: 021565-078

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;  CURRENT APPLICATION NUMBER: US/10/809,953
;  CURRENT FILING DATE:  2004-03-26
;  PRIOR APPLICATION NUMBER: US/09/661,016
;  PRIOR FILING DATE: 2000-09-13
;  PRIOR APPLICATION NUMBER: PCT/EP90/00905
;  PRIOR FILING DATE: 1990-05-30
;  PRIOR APPLICATION NUMBER: GB 89401499.2
;  PRIOR FILING DATE: 1989-05-31
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 1228
;   TYPE: PRT
;   ORGANISM: Bacillus thuringiensis
US-10-809-953-10

  Query Match             88.6%;  Score 5742;  DB 16;  Length 1228;
  Best Local Similarity   89.1%;  Pred. No. 0;
  Matches 1098;  Conservative   35;  Mismatches   90;  Indels   10;  Gaps    3;

Qy          1 LTSNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
              |||||||||||||     |||||| |||| ||||||||||||||||:| ||||||||||
Db          1 LTSNRKNENEIIN-----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGI 55

Qy         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 120
              ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db         56 NIAGRILGVLGVPFAGQLASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 115

Qy        121 LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 180
              ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        116 LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLHTQYIALELDFLNAMPLFAIRNQEVP 175

Qy        181 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLN 240
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db        176 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVERTRDYSDYCVEWYNTGLN 235

Qy        241 SLRGTNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 SLRGTNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG 295

Qy        301 VNMASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQ 360
              |||||||||||||||||| | |||||||||||||||| ||||| ||||||||||||||
Db        296 VNMASMNWYNNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQ 355

Qy        361 SRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFN 420
              |||||||||||||:|||||||| | | ||||| ||||||||||||||||||||||||||
Db        356 SRPIGGGLNTSTHGATNTSINPVTLRFASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFN 415

Qy        421 FRNPQNTFERGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLISQSR 480
              | ||||  :||||||||||||||||||||||||||||||||||||||||||||:| |||
Db        416 FTNPQNISDRGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGIILQSR 475

Qy        481 VHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGS 540
              |:|||||||||||||||  : |||||:||:  |  ||:|| |||||||||:|    |
Db        476 VNVPVYSWTHRSADRTNTIGPNRITQIPMVKASELPQGTTVVRGPGFTGGDILRRTNTGG 535

Qy        541 VLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFR 600
              : :  |    ||||:  |||::      |: ||:|  :  |  ||:: : |   :|
Db        536 FGPIRVTVNGPLTQRYRIGFRYASTVDFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFV 595

Qy        601 FAEPPVGISASGSQ-TAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNAL 659
              |   : :  |     ||   :|    : |||| ||:|||||||||||||||||||||||
Db        596 RRAPTTPFTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFEAEYDLERAQEAVNAL 655

Qy        660 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDP 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDP 715

Qy        720 NFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNEC 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 NFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNEC 775

Qy        780 YPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVE 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        776 YPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVE 835

Qy        840 SPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVF 899
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        836 SPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDVGCTDLHENLGVWVVF 895

Qy        900 KIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVD 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 KIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVD 955

Qy        960 ALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITAI 1019
              ||||||||:|||||||||||||||||||||||||||||| ||||||||||||| |||||
Db        956 ALFVDSQYDRLQADTNIGMIHAADKLVHRIREAYLSELPVIPGVNAEIFEELEGHIITAI 1015

Qy       1020 SLYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYI 1079
              |||||||||||||||| |||||||||||||||| |||||||||||||||||| |||
Db       1016 SLYDARNVVKNGDFNNGLTCWNVKGHVDVQQSHHRSDLVIPEWEAEVSQAVRVCPGCGYI 1075

Qy       1080 LRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTA----V 1135
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1076 LRVTAYKEGYGEGCVTIHEIENNTDELKFKNREEEEVYPTDTGTCNDYTAHQGTAGCADA 1135

Qy       1136 CNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKE 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||:|||
Db       1136 CNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPVPAGYVTKE 1195

Qy       1196 LEYFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
              |||||||| |||||||||||||||||||||||
Db       1196 LEYFPETDTVWIEIGETEGKFIVDSVELLLMEE 1228


RESULT 6
US-09-988-462-7
; Sequence 7, Application US/09988462
; Publication No. US20030046726A1
;   GENERAL INFORMATION:
;        APPLICANT: Koziel, Michael G.
;                   Desai, Nalini M.
;                   Lewis, Kelly S.
;                   Kramer, Vance C.
;                   Warren, Gregory W.
;                   Evola, Stephen V.
;                   Crossland, Lyle D.
;                   Wright, Martha S.
;                   Merlin, Ellis J.
;                   Launis, Karen L.
;        TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;                            INSECTICIDAL ACTIVITY IN MAIZE
;        NUMBER OF SEQUENCES: 94
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Syngenta Biotechnology, Inc.
;             STREET: 3054 Cornwallis Road
;             CITY: Research Triangle Park
;             STATE: NC
;             COUNTRY: USA
;             ZIP: 27709
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/988,462
;             FILING DATE: 20-No. US20030046726A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 09/547,422
;             FILING DATE: 11-APR-2000
;             APPLICATION NUMBER: US 08/459,504
;             FILING DATE: 02-JUN-1995
;             APPLICATION NUMBER: US 07/951,715
;             FILING DATE: 25-SEP-1992
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;             APPLICATION NUMBER: US 07/772,027
;             FILING DATE: 04-OCT-1991
;          ATTORNEY/AGENT INFORMATION:
;             NAME: Meigs, J. Timothy
;             REGISTRATION NUMBER: 38,241
;             REFERENCE/DOCKET NUMBER: S-18805I
;          TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (919)541-8587
;             TELEFAX: (919)541-8689
;    INFORMATION FOR SEQ ID NO: 7:
;          SEQUENCE CHARACTERISTICS:
;             LENGTH: 1207 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-988-462-7

  Query Match             87.4%;  Score 5659.5;  DB 10;  Length 1207;
  Best Local Similarity   89.4%;  Pred. No. 0;
  Matches 1079;  Conservative   34;  Mismatches   89;  Indels    5;  Gaps    2;

Qy         27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRILGVLGVPFAGQIASFYSFLV 86
              ||| |||||||||||||||:| |||||||||||||||||||||||||||:||||||||
Db          1 MDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLV 60

Qy         87 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 120

Qy        147 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEF 180

Qy        207 GLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 266
              |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db        181 GLTSQEIQRYYERQVERTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLD 240

Qy        267 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIETAVIRS 326
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||| |
Db        241 LVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSFSAIEAAAIRS 300

Qy        327 PHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPIGGGLNTSTHGSTNTSINPVRLS 386
              ||||||||||||| ||||| |||||||||||||||||||||||:|||||||| |
Db        301 PHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLR 360

Qy        387 FFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFNFRNPQNTFERGTANYSQPYESPGLQL 446
              | ||||| |||||||||||||||||||||||||| ||||  :|||||||||||||||||
Db        361 FASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNISDRGTANYSQPYESPGLQL 420

Qy        447 KDSETELPPETTERPNYESYSHRLSHIGLISQSRVHVPVYSWTHRSADRTNTISSDSITQ 506
              |||||||||||||||||||||||||:| ||||:||||||||||||  : |||
Db        421 KDSETELPPETTERPNYESYSHRLSHIGIILQSRVNVPVYSWTHRSADRTNTIGPNRITQ 480

Qy        507 IPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ 566
              ||:||:  |  ||:|| |||||||||:|    |    : :  |    ||||:  |||::
Db        481 IPMVKASELPQGTTVVRGPGFTGGDILRRTNTGGFGPIRVTVNGPLTQRYRIGFRYASTV 540

Qy        567 TMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFRFAEFPVGISASGSQ-TAGISISNNAG 625
                  |: ||:|  :  |  ||:: : |   :|    |    : :  |     ||   :|
Db        541 DFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTTPFTFTQIQDIIRTSIQGLSG 600

Qy        626 RQTFHFDKIEFIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 685
              :  |||| ||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NGEVYIDKIEIIPVTATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 660

Qy        686 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ 720

Qy        746 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI 780

Qy        806 EDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 865
              |||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db        781 EDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 840

Qy        866 RDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 925
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        841 RDGEKCAHHSHHFSLDIDVGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA 900

Qy        926 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKL 985
              |||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db        901 LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHAADKL 960

Qy        986 VHRIREAYLSELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGH 1045
              |||||||||||| |||||||||||||| |||||||||||||||||||| |||||||
Db        961 VHRIREAYLSELPVIPGVNAEIFEELEGHIITAISLYDARNVVKNGDFNNGLTCWNVKGH 1020

Qy       1046 VDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDE 1105
              |||||||||| |||||||||||||||| |||||||||||||||||||||||||||||||
Db       1021 VDVQQSHHRSDLVIPEWEAEVSQAVRVCPGCGYILRVTAYKEGYGEGCVTIHEIENNTDE 1080

Qy       1106 LKFKNCEEEEVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAYEVDTTASVNYKPTY 1161
              |||||  |||||||||||||||||||||||      |||||||||||||||||||||||||
Db       1081 LKFKNREEEEVYPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVNYKPTY 1140

Qy       1162 EEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSV 1221
              |||||||||||||||||||||||:||||:|||||||||| ||||||||||||||||||
Db       1141 EEETYTDVRRDNHCEYDRGYVNYPPVPAGYVTKELEYFPETDTVWIEIGETEGKFIVDSV 1200

Qy       1222 ELLLMEE 1228
              |||||||
Db       1201 ELLLMEE 1207


RESULT 7
US-09-826-660-23
; Sequence 23, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
;  APPLICANT: Cardineau, Guy A.
;  APPLICANT:  Stelman, Steven J.
;  APPLICANT:  Narva, Kenneth E.
;  TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
;  FILE REFERENCE: MA-714XC2D1
;  CURRENT APPLICATION NUMBER: US/09/826,660
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 09/178,252
;  PRIOR FILING DATE: 1998-10-23
;  PRIOR APPLICATION NUMBER: 60/065,215
;  PRIOR FILING DATE: 1997-11-12
;  PRIOR APPLICATION NUMBER: 60/076,445
;  PRIOR FILING DATE: 1998-03-02
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
;   LENGTH: 1186
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23

  Query Match             78.8%;  Score 5108;  DB 9;  Length 1186;
  Best Local Similarity   80.6%;  Pred. No. 0;
  Matches  995;  Conservative   76;  Mismatches  108;  Indels   56;  Gaps    8;

Qy          1 LTSNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
              :|||||||||||||||||||| ||:|| |||||||||||||||:| ||||||||||
Db          1 MTSNRKNENEIINALSIPAVSNHSAQMNLSTDARIEDSLCIAEGNNIDPFVSASTVQTGI 60

Qy         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 120
              |||||||||||||||||||||||||||||||||||| |||||||||| ||:||| |:||
Db         61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDPWEIFLEHVEQLIRQQVTENTRDTA 120
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Qy       121 LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 180
Db       121 LARLQGLGNSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP 180

Qy       181 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLN 240
Db       181 LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEKTREYSDYCARWYNTGLN 240

Qy       241 SLRGTNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG 300
Db       241 NLRGTNAESWLRYNQFRRDLTLGVLDLVALFPSYDTRVYPMNTSAQLTREIYTDPIGRTN 300

Qy       301 V--NMASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHT 358
Db       301 APSGFASTNWFNNNAPSFSAIEAAVIRPPHLLDFPEQLTIFSVLSRWSNTQYMNYWVGHR 360

Qy       359 IQSRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTVR 418
Db       361 LESRTIRGSLSTSTHGNTNTSINPVTLQFTSRDVYRTESFAGINI--LLTTPVNGVPWAR 418

Qy       419 FNFRNPQNTFERGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLISQ 478
Db       419 FNWRNPLNSL-RGSLLYTIGYTGVGTQLFDSETELPPETTERPNYESYSHRLSNIRLISG 477

Qy       479 SRVHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVN 538
Db       478 NTLRAPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVN 537

Qy       539 GSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQS 598
Db       538 GSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQS 597

Qy       599 FRFAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNA 658
Db       598 FRFAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATLEAESDLERAQKAVNA 657

Qy       659 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 718
Db       658 LFTSSNQIGLKTDVTDYHIDRVSNLVECLSDEFCLDEKKELSEKVKHAKRLSDERNLLQD 717

Qy       719 PNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNE 778
Db       718 PNFRGINRQLD-----------------RGWRGSTDITIQGGDDVFKENYVTLLGTFDE 759

Qy       779 CYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSV 838
Db       760 CYPTYLYQKIDESKLKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETVNVPGTGSLWPLSA 819

Qy       839 ESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVV 898
Db       820 PSPIG-------------------------KCAHHSHHFSLDIDVGCTDLNEDLGVWVI 853

Qy       899 FKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAV 958
Db       854 FKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESV 913

Qy       959 DALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITA 1018
Db       914 DALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTA 973

Qy      1019 ISLYDARNVVKNGDFNNGLACWNVKGHVDV-QQSHHRSVLVIPEWEAEVSQAVRVCPGRG 1077
Db       974 FSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNHRSVLVVPEWEAEVSQEVRVCPGRG 1033

Qy      1078 YILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTA----HQGT 1133
Db       1034 YILRVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEVYPNNTVTCNDYTATQEEYEGT 1093

Qy      1134 AVCNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYMT 1193
Db       1094 --YTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESNRGYGDYTPLPAGYVT 1151

Qy      1194 KELEYFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
Db       1152 KELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1186
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RESULT 8
US-09-972-175-59
; Sequence 59, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Gilmer, Amy Jelen
; Mettus, Anne-Marie Light
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,175
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/337,635
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MECO:206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-972-175-59

Query Match 54.1%; Score 3502.5; DB 10; Length 1189;
Best Local Similarity 57.0%; Pred. No. 2e-259;
Matches 717; Conservative 143; Mismatches 289; Indels 109; Gaps 20;

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Qy         7 NENEII--NALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAG 64
Db         5 NQNQCIPYNCLS-------------NPEEVLLDGERISTGN--------SSIDISLSLVQ 43

Qy        65 RILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTALARL 124
Db        44 FLVSNF-VPGGGFLVGLIDFVWGIVGP---SQWDAFLVQIEQLINERIAEFARNAAIANL 99

Qy       125 QGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMV 184
Db       100 EGLGNNFNIYVEAFKEWEEDPNNPATRTRVIDRFRILDGLLERDIPSFAISGFEVPLLSV 159

Qy       185 YAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRG 244
Db       160 YAQAANLHLAILRDSVIFGERWGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNNLPA 219

Qy       245 TNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMA 304
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Db        220 STYQDWITYNRLRRDLTLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPL----INFN 275

Qy        305 SMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPI 364
                  |:|: :|:: ||:||| | |  ||||:    | :     || || : |  |
Db        276 PQLQSVAQLPTFNVMESSAIRNPHLFDILNNLTIFTD---WFSVGRNFYWGGHRVISSLI 332

Qy        365 GGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLL----WGIYLEPIHGVPTVRFN 420
              |||  ||       :  | |   |:  |: | |  : |    |      : ||  | |:
Db        333 GGGNITSPIYGREANQEPPRSFTFNGPVFRTLSNPTLRLLQQPWPAPPFNLRGVEGVEFS 392

Qy        421 FRNPQNTFE---RGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLIS 477
                 | |:|    |||               || ||||||    |  | ||||| |   :
Db        393 --TPTNSFTYRGRGTV-------------DSLTELPPEDNSVPPREGYSHRLCHATFVQ 436

Qy        478 QSRVHV----PVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDII 533
              :|         |:|||||| |||| : | |||||| | :  ||||::|||||||||:
Db        437 RSGTPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDIL 496

Qy        534 RTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ-------TMVLRVTVGGSTTFDQGFPS 586
              | |  |  :|: :| |:   ||||:| |||:|:       |      |||  : :
Db        497 RRNTFGDFVSLQVNINSPITQRYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQK 556

Qy        587 TMSANESLTSQSFRFAEFP----------VGISASGSQTAGISISNNAGRQTFHFDKIE 635
              ||   |:|||::||: :|           :|||      || |||:       : ||||
Db        557 TMEIGENLTSRTFRYTDFSNPFSFRANPDIIGISEQPLFGAG-SISSG----ELYIDKIE 611

Qy        636 FIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDE 695
               |   |||||| |||||:|||||::|   |||||||||||||||| ||||||||||
Db        612 IILADATFEAESDLERAQKAVNALFTSSNQIGLKTDVTDYHIDQVSNLVDCLSDEFCLDE 671

Qy        696 KRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSEN 755
              |||| ||||:|||||||||||||||  ||:|||                || || :
Db        672 KRELSEKVKHAKRLSDERNLLQDPNFRGINRQPD-----------------RGWRGSTD 713

Qy        756 ITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYL 815
              |||| |:||||||||||||| :||||||||||| ||:|||||||:|||||||||||||||
Db        714 ITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLKAYTRYELRGYIEDSQDLEIYL 773

Qy        816 IRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHS 875
              |||||||| ::|||| |:|||| :||||:|||||||||| ||||||||||||||||||||
Db        774 IRYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHHS 833

Qy        876 HHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKK 935
              |||:|||||||||:|:|||||:||||||:||||||||||:||||||||:||||||||
Db        834 HHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLLGEALARVKRAEKK 893

Qy        936 WRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLS 995
              |||||||||||  || ||||:||||||:|||:||| |||| |||||||| |||||||||
Db        894 WRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIAMIHAADKRVHRIREAYLP 953

Qy        996 ELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGHVDV-QQSHHR 1054
              |||||||||| |||||||| || |||||||:|||||||| |||||||||| :|::||
Db        954 ELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGLLCWNVKGHVDVEEQNNHR 1013

Qy       1055 SVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEE 1114
              |||||||||||||| ||||||||||||||||||||||||||||:||||||| || ||
Db       1014 SVLVIPEWEAEVSQEVRVCPGRGYILRVTAYKEGYGEGCVTIHEIEDNTDELKFSNCVEE 1073

Qy       1115 EVYPTDTGTCNDYTA----HQGTAVCNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVR 1170
              |||| :| |||:||     ::||    ||| ||::||  : :   :|   |||::||| |
Db       1074 EVYPNNTVTCNNYTGTQEEYEGT--YTSRNQGYDEAYGNNPSVPADYASVYEEKSYTDGR 1131

Qy       1171 RDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
              |:| || :||| :| |||||:||:||||||||||||||||| ||||||||||
Db       1132 RENPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1189


RESULT 9
US-10-200-522-59
; Sequence 59, Application US/10200522
; Publication No. US20030195336A1
; GENERAL INFORMATION:
;  APPLICANT: Baum, James A.
;  APPLICANT:  Gilmer, Amy Jelen
;  APPLICANT:  Mettus, Anne Marie Light
;  TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE COMPOSITIONS ENCODING LEPIDOPTERAN-TC
;  TITLE OF INVENTION:  POLYPEPTIDES
;  FILE REFERENCE: MECO:213 (11792.0213 DVUS01)
;  CURRENT APPLICATION NUMBER: US/10/200,522
;  CURRENT FILING DATE:  2002-07-22
;  PRIOR APPLICATION NUMBER: 09/337,280
;  PRIOR FILING DATE: 1999-06-22
;  PRIOR APPLICATION NUMBER: 08/980,071
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: 08/757,536
;  PRIOR FILING DATE: 1996-11-27
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
;   LENGTH: 1189
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant Delta Endotoxin
US-10-200-522-59

  Query Match           54.1%;  Score 3502.5;  DB 14;  Length 1189;
  Best Local Similarity  57.0%;  Pred. No. 2e-259;
  Matches  717;  Conservative  143;  Mismatches  289;  Indels  109;  Gaps   20;

Qy          7 NENEII--NALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAG 64
                |:|: |  | ||           :|:  : |   |: ||        |::   :::
Db          5 NQNQCIPYNCLS-------------NPEEVLLDGERISTGN--------SSIDISLSLVQ 43

Qy         65 RILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTALARL 124
                ::    ||  | :     |: | : |    ||: ||  :|||||::| | ||| |:| |
Db         44 FLVSNF-VPGGGFLVGLIDFVWGIVGP---SQWDAFLVQIEQLINERIAEFARNAAIANL 99

Qy        125 QGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMV 184
              :|||::|  | :: ::| |: ::  ||: :  ::  |:      :| |||   ||||| |
Db        100 EGLGNNFNIYVEAFKEWEEDPNNPATRTRVIDRFRILDGLLERDIPSFAISGFEVPLLSV 159

Qy        185 YAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRG 244
              ||||||||| :|||: :||  :|||:  :    | | :     :|:|:|    || |||:|
Db        160 YAQAANLHLAILRDSVIFGERWGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNNLPA 219

Qy        245 TNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMA 304
              :    |: ||: |||||| |||: | ||:|| | |||     |||||||| :     :|
Db        220 STYQDWITYNRLRRDLTLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPL----INFN 275

Qy        305 SMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPI 364
                      |:|: :|:: ||:||| | |  ||||:    | :     || || : |  |
Db        276 PQLQSVAQLPTFNVMESSAIRNPHLFDILNNLTIFTD---WFSVGRNFYWGGHRVISSLI 332

Qy        365 GGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLL----WGIYLEPIHGVPTVRFN 420
              |||  ||       :  | |   |:  |: | |  : |    |      : ||  | |:
Db        333 GGGNITSPIYGREANQEPPRSFTFNGPVFRTLSNPTLRLLQQPWPAPPFNLRGVEGVEFS 392

Qy        421 FRNPQNTFE---RGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLIS 477
                 | |:|    |||               || ||||||    |  | ||||| |   :
Db        393 --TPTNSFTYRGRGTV-------------DSLTELPPEDNSVPPREGYSHRLCHATFVQ 436

Qy        478 QSRVHV----PVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDII 533
              :|         |:|||||| |||| : | |||||| | :  ||||::|||||||||:
Db        437 RSGTPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDIL 496

Qy        534 RTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ-------TMVLRVTVGGSTTFDQGFPS 586
              | |  |  :|: :| |:   ||||:| |||:|:       |      |||  : :
Db        497 RRNTFGDFVSLQVNINSPITQRYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQK 556

Qy        587 TMSANESLTSQSFRFAEFP----------VGISASGSQTAGISISNNAGRQTFHFDKIE 635
              ||   |:|||::||: :|           :|||      || |||:       : ||||
Db        557 TMEIGENLTSRTFRYTDFSNPFSFRANPDIIGISEQPLFGAG-SISSG----ELYIDKIE 611

Qy        636 FIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDE 695
               |   |||||| |||||:|||||::|   |||||||||||||||| ||||||||||
Db        612 IILADATFEAESDLERAQKAVNALFTSSNQIGLKTDVTDYHIDQVSNLVDCLSDEFCLDE 671
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Db        612 IILADATFEAESDLERAQKAVNALFTSSNQIGLKTDVTDYHIDQVSNLVDCLSDEFCLDE 671

Qy        696 KRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSEN 755
              |||| |||||:|||||||||||||||||  ||:|||                    || || :
Db        672 KRELSEKVKHAKRLSDERNLLQDPNFRGINRQPD-----------------RGWRGSTD 713

Qy        756 ITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYL 815
              |||| |:||||||||||||| :|||||||||| ||:|||||||:|||||||||||||||
Db        714 ITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLKAYTRYELRGYIEDSQDLEIYL 773

Qy        816 IRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHS 875
              |||||||| ::|||| |:|||| :||||:|||||||||| ||||||||||||||||||||
Db        774 IRYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHHS 833

Qy        876 HHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKK 935
              |||:||||:|||||:|:|||||:||||||:||||||||||:||||||||||:|||||||
Db        834 HHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLLGEALARVKRAEKK 893

Qy        936 WRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLS 995
              |||||||||||  || ||||:||||||:|||:||| |||| |||||||| |||||||||
Db        894 WRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIAMIHAADKRVHRIREAYLP 953

Qy        996 ELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGHVDV-QQSHHR 1054
              |||||||||| |||||||| || ||||||||:|||||||| |||||||||| :|::||
Db        954 ELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGLLCWNVKGHVDVEEQNNHR 1013

Qy       1055 SVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEE 1114
              |||||||||||||| ||||||||||||||||||||||||||||:||||||| || ||
Db       1014 SVLVIPEWEAEVSQEVRVCPGRGYILRVTAYKEGYGEGCVTIHEIEDNTDELKFSNCVEE 1073

Qy       1115 EVYPTDTGTCNDYTA----HQGTAVCNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVR 1170
              |||| :| |||:||     ::||    ||| ||::||  : :   :|   |||::||| |
Db       1074 EVYPNNTVTCNNYTGTQEEYEGT--YTSRNQGYDEAYGNNPSVPADYASVYEEKSYTDGR 1131

Qy       1171 RDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
              |:| || :||| :| |||||||:||:||||||||||||||||| ||||||||||||
Db       1132 RENPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1189


RESULT 10
US-09-972-175-2
; Sequence 2, Application US/09972175
; Publication No. US20030101482A1
;   GENERAL INFORMATION:
;        APPLICANT: Baum, James A.
;                   Gilmer, Amy Jelen
;                   Mettus, Anne-Marie Light
;        TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
;                            LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
;        NUMBER OF SEQUENCES: 76
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Arnold, White & Durkee
;             STREET: P.O. Box 4433
;             CITY: Houston
;             STATE: Texas
;             COUNTRY: USA
;             ZIP: 77210
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/972,175
;             FILING DATE: 05-Oct-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/337,635
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kitchell, Barbara S.
;             REGISTRATION NUMBER: 33,928
;             REFERENCE/DOCKET NUMBER: MECO:206
;             TELECOMMUNICATION INFORMATION:
;                  TELEPHONE: 512/418-3000
;                  TELEFAX: 512/474-7577
;        INFORMATION FOR SEQ ID NO: 2:
;             SEQUENCE CHARACTERISTICS:
;                  LENGTH: 1189 amino acids
;                  TYPE: amino acid
;                  TOPOLOGY: linear
;             MOLECULE TYPE: protein
;             SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-972-175-2

  Query Match             54.0%;  Score 3500.5;  DB 10;  Length 1189;
  Best Local Similarity   57.0%;  Pred. No. 2.8e-259;
  Matches  717;  Conservative  143;  Mismatches  289;  Indels  109;  Gaps   20;

Qy          7 NENEII--NALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAG 64
              |:|: |  | ||             :|:  : |   |: ||        |::   :::
Db          5 NQNQCIPYNCLS------------NPEEVLLDGERISTGN--------SSIDISLSLVQ 43

Qy         65 RILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTALARL 124
               ::    ||  | :      |: | : |    ||: ||  :|||||::| | ||| |:| |
Db         44 FLVSNF-VPGGGFLVGLIDFVWGIVGP---SQWDAFLVQIEQLINERIAEFARNAAIANL 99

Qy        125 QGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMV 184
              :|||::|  | :: ::| |: ::  ||: :  ::  |:      :| |||   ||||| |
Db        100 EGLGNNFNIYVEAFKEWEEDPNNPATRTRVIDRFRILDGLLERDIPSFAISGFEVPLLSV 159

Qy        185 YAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRG 244
              |||||||| :|||: :||  :|||:  :   | | :    :|:|:|   || |||:|
Db        160 YAQAANLHLAILRDSVIFGERWGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNNLPK 219

Qy        245 TNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMA 304
              :    |: ||: |||||| |||: | ||:|| | |||     ||||||||| :    :|
Db        220 STYQDWITYNRLRRDLTLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPL----INFN 275

Qy        305 SMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPI 364
                      |:|: :|:: ||:||| | |  ||||:    | :    || || : |  |
Db        276 PQLQSVAQLPTFNVMESSAIRNPHLFDILNNLTIFTD---WFSVGRNFYWGGHRVISSLI 332

Qy        365 GGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLL----WGIYLEPIHGVPTVRFN 420
              |||  ||       :  | |   |:  |: | |   : |    |      : ||  | |:
Db        333 GGGNITSPIYGREANQEPPRSFTFNGPVFRTLSNPTLRLLQQPWPAPPFNLRGVEGVEFS 392

Qy        421 FRNPQNTFE---RGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLIS 477
                | |:|   |||                || ||||||   |  | |||| |   :
Db        393 --TPTNSFTYRGRGTV-------------DSLTELPPEDNSVPPREGYSHRLCHATFVQ 436

Qy        478 QSRVHV----PVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDII 533
              :|         |:|||||| ||||  : | |||||| | :  ||||::||||||||:
Db        437 RSGTPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDIL 496

Qy        534 RTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ-------TMVLRVTVGGSTTFDQGFPS 586
              | |  |  :|: :| |:   ||||:| |||:|:        |      |||  : :
Db        497 RRNTFGDFVSLQVNINSPITQRYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQK 556

Qy        587 TMSANESLTSQSFRFAEFP-----------VGISASGSQTAGISISNNAGRQTFHFDKIE 635
              ||   |:|||::||: :|              :|||    || |||:       : ||||
Db        557 TMEIGENLTSRTFRYTDFSNPFSFRANPDIIGISEQPLFGAG-SISSG----ELYIDKIE 611

Qy        636 FIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDE 695
              |   |||||| ||||||:|||||||::|   |||||||||||||| ||||||||||||||
Db        612 IILADATFEAESDLERAQKAVNALFTSSNQIGLKTDVTDYHIDQVSNLVDCLSDEFCLDE 671

Qy        696 KRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSEN 755
              |||| ||||:|||||||||||||||  ||:|||                    || || :
Db        672 KRELSEKVKHAKRLSDERNLLQDPNFRGINRQPD-----------------RGWRGSTD 713

Qy        756 ITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYL 815
              |||| |:||||||||||||| :|||||||||| ||:|||||||:|||||||||||||||
Db        714 ITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLKAYTRYELRGYIEDSQDLEIYL 773

Qy        816 IRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHS 875
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Db        774 IRYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHHS 833

Qy        876 HHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKK 935
Db        834 HHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLLGEALARVKRAEKK 893

Qy        936 WRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLS 995
Db        894 WRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIAMIHAADKRVHRIREAYLP 953

Qy        996 ELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGHVDV-QQSHHR 1054
Db        954 ELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGLLCWNVKGHVDVEEQNNHR 1013

Qy       1055 SVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEE 1114
Db       1014 SVLVIPEWEAEVSQEVRVCPGRGYILRVTAYKEGYGEGCVTIHEIEDNTDELKFSNCVEE 1073

Qy       1115 EVYPTDTGTCNDYTA----HQGTAVCNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVR 1170
Db       1074 EVYPNNTVTCNNYTGTQEEYEGT--YTSRNQGYDEAYGNNPSVPADYASVYEEKSYTDGR 1131

Qy       1171 RDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
Db       1132 RENPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1189


RESULT 11
US-10-200-522-2
; Sequence 2, Application US/10200522
; Publication No. US20030195336A1
; GENERAL INFORMATION:
;  APPLICANT: Baum, James A.
;  APPLICANT:  Gilmer, Amy Jelen
;  APPLICANT:  Mettus, Anne Marie Light
;  TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE COMPOSITIONS ENCODING LEPIDOPTERAN-T
;  TITLE OF INVENTION:  POLYPEPTIDES
;  FILE REFERENCE: MECO:213 (11792.0213 DVUS01)
;  CURRENT APPLICATION NUMBER: US/10/200,522
;  CURRENT FILING DATE:  2002-07-22
;  PRIOR APPLICATION NUMBER: 09/337,280
;  PRIOR FILING DATE: 1999-06-22
;  PRIOR APPLICATION NUMBER: 08/980,071
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: 08/757,536
;  PRIOR FILING DATE: 1996-11-27
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 1189
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant Delta Endotoxin
US-10-200-522-2

  Query Match           54.0%;  Score 3500.5;  DB 14;  Length 1189;
  Best Local Similarity  57.0%;  Pred. No. 2.8e-259;
  Matches  717;  Conservative  143;  Mismatches  289;  Indels  109;  Gaps   20;

Qy          7 NENEII--NALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAG 64
Db          5 NQNQCIPYNCLS------------NPEEVLLDGERISTGN--------SSIDISLSLVQ 43

Qy         65 RILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTALARL 124
Db         44 FLVSNF-VPGGGFLVGLIDFVWGIVGP---SQWDAFLVQIEQLINERIAEFARNAAIANL 99

Qy        125 QGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMV 184
Db        100 EGLGNNFNIYVEAFKEWEEDPNNPATRTRVIDRFRILDGLLERDIPSFAISGFEVPLLSV 159

Qy        185 YAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRG 244
Db        160 YAQAANLHLAILRDSVIFGERWGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNNLPK 219

Qy        245 TNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMA 304
Db        220 STYQDWITYNRLRRDLTLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPL----INFN 275

Qy        305 SMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPI 364
Db        276 PQLQSVAQLPTFNVMESSAIRNPHLFDILNNLTIFTD---WFSVGRNFYWGGHRVISSLI 332

Qy        365 GGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLL----WGIYLEPIHGVPTVRFN 420
Db        333 GGGNITSPIYGREANQEPPRSFTFNGPVFRTLSNPTLRLLQQPWPAPPFNLRGVEGVEFS 392

Qy        421 FRNPQNTFE---RGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLIS 477
Db        393 --TPTNSFTYRGRGTV--------------DSLTELPPEDNSVPPREGYSHRLCHATFVQ 436

Qy        478 QSRVHV----PVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDII 533
Db        437 RSGTPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDIL 496

Qy        534 RTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ-------TMVLRVTVGGSTTFDQGFPS 586
Db        497 RRNTFGDFVSLQVNINSPITQRYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQK 556

Qy        587 TMSANESLTSQSFRFAEFP-----------VGISASGSQTAGISISNNAGRQTFHFDKIE 635
Db        557 TMEIGENLTSRTFRYTDFSNPFSFRANPDIIGISEQPLFGAG-SISSG----ELYIDKIE 611

Qy        636 FIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDE 695
Db        612 IILADATFEAESDLERAQKAVNALFTSSNQIGLKTDVTDYHIDQVSNLVDCLSDEFCLDE 671

Qy        696 KRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSEN 755
Db        672 KRELSEKVKHAKRLSDERNLLQDPNFRGINRQPD-----------------RGWRGSTD 713

Qy        756 ITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYL 815
Db        714 ITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLKAYTRYELRGYIEDSQDLEIYL 773

Qy        816 IRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHS 875
Db        774 IRYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHHS 833

Qy        876 HHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKK 935
Db        834 HHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLLGEALARVKRAEKK 893

Qy        936 WRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLS 995
Db        894 WRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIAMIHAADKRVHRIREAYLP 953

Qy        996 ELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGHVDV-QQSHHR 1054
Db        954 ELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGLLCWNVKGHVDVEEQNNHR 1013

Qy       1055 SVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEE 1114
Db       1014 SVLVIPEWEAEVSQEVRVCPGRGYILRVTAYKEGYGEGCVTIHEIEDNTDELKFSNCVEE 1073

Qy       1115 EVYPTDTGTCNDYTA----HQGTAVCNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVR 1170
Db       1074 EVYPNNTVTCNNYTGTQEEYEGT--YTSRNQGYDEAYGNNPSVPADYASVYEEKSYTDGR 1131

Qy       1171 RDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
Db       1132 RENPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1189
```

```
RESULT 12
US-09-972-175-61
; Sequence 61, Application US/09972175
; Publication No. US20030101482A1
;  GENERAL INFORMATION:
;       APPLICANT: Baum, James A.
;                  Gilmer, Amy Jelen
;                  Mettus, Anne-Marie Light
;       TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
;                           LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
;       NUMBER OF SEQUENCES: 76
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Arnold, White & Durkee
;            STREET: P.O. Box 4433
;            CITY: Houston
;            STATE: Texas
;            COUNTRY: USA
;            ZIP: 77210
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/972,175
;            FILING DATE: 05-Oct-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/337,635
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Kitchell, Barbara S.
;            REGISTRATION NUMBER: 33,928
;            REFERENCE/DOCKET NUMBER: MECO:206
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 512/418-3000
;            TELEFAX: 512/474-7577
;  INFORMATION FOR SEQ ID NO: 61:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1189 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-09-972-175-61

  Query Match             54.0%;  Score 3496.5;  DB 10;  Length 1189;
  Best Local Similarity   56.9%;  Pred. No. 5.8e-259;
  Matches  716;  Conservative  143;  Mismatches  290;  Indels  109;  Gaps   20;

Qy          7 NENEII--NALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAG 64
              |:|: |  | ||           :|:  : |   |: ||        |::   :::
Db          5 NQNQCIPYNCLS-----------NPEEVLLDGERISTGN--------SSIDISLSLVQ 43

Qy         65 RILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTALARL 124
               ::    ||  | :     |: | : |    ||: ||  :|||||::| | ||| |:| |
Db         44 FLVSNF-VPGGGFLVGLIDFVWGIVGP---SQWDAFLVQIEQLINERIAEFARNAAIANL 99

Qy        125 QGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMV 184
              :|||::|  | :: ::| |: ::  ||: :  ::  |:      :| | |   |||| |
Db        100 EGLGNNFNIYVEAFKEWEEDPNNPATRTRVIDRFRILDGLLERDIPSFDISGFEVPLLSV 159

Qy        185 YAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRG 244
              ||||||||| :|||: :||  :|||:  :    | | :    :|:|:|   || |||:|
Db        160 YAQAANLHLAILRDSVIFGERWGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNNLPA 219

Qy        245 TNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMA 304
              :    |: ||: |||||| |||: | ||:|| | |||    ||||||||| :    :|
Db        220 STYQDWITYNRLRRDLTLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPL----INFN 275

Qy        305 SMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPI 364
                        |:|: :|:: ||:||| | |  ||||:    | :      || || : |  |
Db        276 PQLQSVAQLPTFNVMESSAIRNPHLFDILNNLTIFTD---WFSVGRNFYWGGHRVISSLI 332

Qy        365 GGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLL----WGIYLEPIHGVPTVRFN 420
              |||  ||       :  | |   |:  |: | |   : |    |      : ||  | |:
Db        333 GGGNITSPIYGREANQEPPRSFTFNGPVFRTLSNPTLRLLQQPWPAPPFNLRGVEGVEFS 392

Qy        421 FRNPQNTFE---RGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLIS 477
                | |:|   |||                || ||||||    |  | |||||  |   :
Db        393 --TPTNSFTYRGRGTV-------------DSLTELPPEDNSVPPREGYSHRLCHATFVQ 436

Qy        478 QSRVHV----PVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDII 533
              :|       |:|||||||  |||| : | |||||| | :  ||||::|||||||||:
Db        437 RSGTPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDIL 496

Qy        534 RTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ-------TMVLRVTVGGSTTFDQGFPS 586
              | |  |  :|: :| |:   ||||:| |||:|:       |      |||  : :
Db        497 RRNTFGDFVSLQVNINSPITQRYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQK 556

Qy        587 TMSANESLTSQSFRFAEFP-----------VGISASGSQTAGISISNNAGRQTFHFDKIE 635
              ||   |:|||::||: :|           :|||       || |||:       : ||||
Db        557 TMEIGENLTSRTFRYTDFSNPFSFRANPDIIGISEQPLFGAG-SISSG----ELYIDKIE 611

Qy        636 FIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDE 695
              |   ||||||:||||||:|||||||::|   |||||||||||||||| ||||||||||
Db        612 IILADATFEAESDLERAQKAVNALFTSSNQIGLKTDVTDYHIDQVSNLVDCLSDEFCLDE 671

Qy        696 KRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSEN 755
              |||| ||||:||||||||||||||  ||:|||                  || || :
Db        672 KRELSEKVKHAKRLSDERNLLQDPNFRGINRQPD-----------------RGWRGSTD 713

Qy        756 ITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYL 815
              |||| |:||||||||||||| :||||||||| ||:|||||||:||||||||||||||
Db        714 ITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLKAYTRYELRGYIEDSQDLEIYL 773

Qy        816 IRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHS 875
              |||||||| ::|||| |:|||| :||||:|||||||||| ||||||||||||||||||||
Db        774 IRYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHHS 833

Qy        876 HHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKK 935
              |||:||||:|||||:|:|||||:||||||:||||||||||:||||||||:||||||||
Db        834 HHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLLGEALARVKRAEKK 893

Qy        936 WRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLS 995
              |||||||||||   || ||||:||||||:|||:||| |||| |||||| |||||||||
Db        894 WRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIAMIHAADKRVHRIREAYLP 953

Qy        996 ELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGHVDV-QQSHHR 1054
              |||||||||| |||||||||:|||||||:|||||||| ||||||||||:|::||
Db        954 ELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGLLCWNVKGHVDVEEQNNHR 1013

Qy       1055 SVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEE 1114
              |||||||||||||| ||||||||||||||||||||||||||||||:|||||| || ||
Db       1014 SVLVIPEWEAEVSQEVRVCPGRGYILRVTAYKEGYGEGCVTIHEIEDNTDELKFSNCVEE 1073

Qy       1115 EVYPTDTGTCNDYTA----HQGTAVCNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVR 1170
              |||| :| |||:||     ::||    ||| ||::||  : :   :|   |||::||| |
Db       1074 EVYPNNTVTCNNYTGTQEEYEGT--YTSRNQGYDEAYGNNPSVPADYASVYEEKSYTDGR 1131

Qy       1171 RDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
              |:| || :||| :| ||||||:||:||||||||||||||||| ||||||||||||
Db       1132 RENPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1189

RESULT 13
US-10-200-522-61
; Sequence 61, Application US/10200522
; Publication No. US20030195336A1
; GENERAL INFORMATION:
;  APPLICANT: Baum, James A.
;  APPLICANT:  Gilmer, Amy Jelen
;  APPLICANT:  Mettus, Anne Marie Light
;  TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE COMPOSITIONS ENCODING LEPIDOPTERAN-T
;  TITLE OF INVENTION:  POLYPEPTIDES
;  FILE REFERENCE: MECO:213 (11792.0213 DVUS01)
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;  CURRENT APPLICATION NUMBER: US/10/200,522
;  CURRENT FILING DATE:  2002-07-22
;  PRIOR APPLICATION NUMBER: 09/337,280
;  PRIOR FILING DATE: 1999-06-22
;  PRIOR APPLICATION NUMBER: 08/980,071
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: 08/757,536
;  PRIOR FILING DATE: 1996-11-27
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1189
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant Delta Endotoxin
US-10-200-522-61

  Query Match             54.0%;  Score 3496.5;  DB 14;  Length 1189;
  Best Local Similarity   56.9%;  Pred. No. 5.8e-259;
  Matches  716;  Conservative  143;  Mismatches  290;  Indels  109;  Gaps   20;

Qy          7 NENEII--NALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAG 64
              |:|: |  | ||              :|:  : |   |: ||        |::   :::
Db          5 NQNQCIPYNCLS------------NPEEVLLDGERISTGN--------SSIDISLSLVQ 43

Qy         65 RILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTALARL 124
               ::    ||  | :     |: | : |    ||: ||  :|||||::| | ||| |:| |
Db         44 FLVSNF-VPGGGFLVGLIDFVWGIVGP---SQWDAFLVQIEQLINERIAEFARNAAIANL 99

Qy        125 QGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMV 184
              :|||::|  | :: ::| |: ::  ||: :  ::  |:      :| | |   ||||| |
Db        100 EGLGNNFNIYVEAFKEWEEDPNNPATRTRVIDRFRILDGLLERDIPSFDISGFEVPLLSV 159

Qy        185 YAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRG 244
              ||||||||| :|||: :||  :|||:  :    | | :    :|:|:|    || |||:|
Db        160 YAQAANLHLAILRDSVIFGERWGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNNLPA 219

Qy        245 TNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMA 304
              :    |: ||: |||||| |||: | ||:|| | |||     |||||||| :    :|
Db        220 STYQDWITYNRLRRDLTLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPL----INFN 275

Qy        305 SMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPI 364
                      |:|: :|:: ||:||| | |  ||||:    | :      || || : |  |
Db        276 PQLQSVAQLPTFNVMESSAIRNPHLFDILNNLTIFTD---WFSVGRNFYWGGHRVISSLI 332

Qy        365 GGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLL----WGIYLEPIHGVPTVRFN 420
              |||  ||       :  | |   |:  |: | |   : |     |       : ||  | |:
Db        333 GGGNITSPIYGREANQEPPRSFTFNGPVFRTLSNPTLRLLQQPWPAPPFNLRGVEGVEFS 392

Qy        421 FRNPQNTFE---RGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLIS 477
                |:|    |||                || ||||||     |  | ||||| |    :
Db        393 --TPTNSFTYRGRGTV-------------DSLTELPPEDNSVPPREGYSHRLCHATFVQ 436

Qy        478 QSRVHV----PVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDII 533
              :|        |:|||||||  ||||  : | |||||| | :  ||||::|||||||||:
Db        437 RSGTPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDIL 496

Qy        534 RTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ-------TMVLRVTVGGSTTFDQGFPS 586
              | |  |  :|: :| |:   ||||:| |||:|:       |       |||  : :
Db        497 RRNTFGDFVSLQVNINSPITQRYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQK 556

Qy        587 TMSANESLTSQSFRFAEFP-----------VGISASGSQTAGISISNNAGRQTFHFDKIE 635
              ||   |:|||::||: :|            :|||      || |||:       : ||||
Db        557 TMEIGENLTSRTFRYTDFSNPFSFRANPDIIGISEQPLFGAG-SISSG----ELYIDKIE 611

Qy        636 FIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDE 695
              |   |||||| ||||||:|||||||::|   |||||||||||||||| ||||||||||
Db        612 IILADATFEAESDLERAQKAVNALFTSSNQIGLKTDVTDYHIDQVSNLVDCLSDEFCLDE 671

Qy        696 KRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSEN 755
              |||| |||||:|||||||||||||||  ||:|||                || || :
Db        672 KRELSEKVKHAKRLSDERNLLQDPNFRGINRQPD-----------------RGWRGSTD 713

Qy        756 ITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYL 815
              |||| |:|||||||||||||| :|||||||||| ||:|||||||:|||||||||||||||
Db        714 ITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLKAYTRYELRGYIEDSQDLEIYL 773

Qy        816 IRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHS 875
              |||||||| ::|||| |:|||| :||||:|||||||||| ||||||||||||||||||||
Db        774 IRYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHHS 833

Qy        876 HHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKK 935
              |||:||||:|||||:|:|||||:||||||:||||||||||:||||||||||:||||||||
Db        834 HHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLLGEALARVKRAEKK 893

Qy        936 WRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLS 995
              |||||||||||  || ||||:||||||:|||:||| |||| |||||||  |||||||||
Db        894 WRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIAMIHAADKRVHRIREAYLP 953

Qy        996 ELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGHVDV-QQSHHR 1054
              |||||||||| |||||||| || ||||||||:|||||||| |||||||||| :|::||
Db        954 ELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGLLCWNVKGHVDVEEQNNHR 1013

Qy       1055 SVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEE 1114
              |||||||||||||| ||||||||||||||||||||||||||||||:|||||| || ||
Db       1014 SVLVIPEWEAEVSQEVRVCPGRGYILRVTAYKEGYGEGCVTIHEIEDNTDELKFSNCVEE 1073

Qy       1115 EVYPTDTGTCNDYTA----HQGTAVCNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVR 1170
              |||| :| |||:||      ::||     ||| ||::||  : :   :|   |||::||| |
Db       1074 EVYPNNTVTCNNYTGTQEEYEGT--YTSRNQGYDEAYGNNPSVPADYASVYEEKSYTDGR 1131

Qy       1171 RDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
              |:| || :||| :| |||||||:||:||||||||||||||||| ||||||||||||
Db       1132 RENPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1189


RESULT 14
US-10-782-020-7
; Sequence 7, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
;  APPLICANT: Carozzi, Nadine
;  APPLICANT:  Hargiss, Tracy
;  APPLICANT:  Koziel, Michael G.
;  APPLICANT:  Duck, Nicholas B.
;  APPLICANT:  Carr, Brian
;  TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
;  TITLE OF INVENTION:  Methods for Its Use
;  FILE REFERENCE: 045600/274139
;  CURRENT APPLICATION NUMBER: US/10/782,020
;  CURRENT FILING DATE:  2004-02-19
;  PRIOR APPLICATION NUMBER: 60/448,810
;  PRIOR FILING DATE: 2003-02-20
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 1189
;   TYPE: PRT
;   ORGANISM: Bacillus thuringiensis
US-10-782-020-7

  Query Match             54.0%;  Score 3495.5;  DB 16;  Length 1189;
  Best Local Similarity   56.9%;  Pred. No. 6.9e-259;
  Matches  716;  Conservative  143;  Mismatches  290;  Indels  109;  Gaps   20;

Qy          7 NENEII--NALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAG 64
              |:|: |  | ||              :|:  : |   |: ||        |::   :::
Db          5 NQNQCIPYNCLS------------NPEEVLLDGERISTGN--------SSIDISLSLVQ 43

Qy         65 RILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTALARL 124
               ::    ||  | :     |: | : |    ||: ||  :|||||::| | ||| |:| |
Db         44 FLVSNF-VPGGGFLVGLIDFVWGIVGP---SQWDAFLVQIEQLINERIAEFARNAAIANL 99

Qy        125 QGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMV 184
              :|||::|  | :: ::| |: ::  ||: :  ::  |:      :| | |   ||||| |
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Db        100 EGLGNNFNIYVEAFKEWEEDPNNPATRTRVIDRFRILDGLLERDIPSFRISGFEVPLLSV 159

Qy        185 YAQAANLHLLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRG 244

Db        160 YAQAANLHLAILRDSVIFGERWGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNNLPK 219

Qy        245 TNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMA 304

Db        220 STYQDWITYNRLRRDLTLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPL----INFN 275

Qy        305 SMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPI 364

Db        276 PQLQSVAQLPTFNVMESSAIRNPHLFDILNNLTIFTD---WFSVGRNFYWGGHRVISSLI 332

Qy        365 GGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLL----WGIYLEPIHGVPTVRFN 420

Db        333 GGGNITSPIYGREANQEPPRSFTFNGPVFRTLSNPTLRLLQQPWPAPPFNLRGVEGVEFS 392

Qy        421 FRNPQNTFE---RGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLIS 477

Db        393 --TPTNSFTYRGRGTV-------------DSLTELPPEDNSVPPREGYSHRLCHATFVQ 436

Qy        478 QSRVHV----PVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDII 533

Db        437 RSGTPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDIL 496

Qy        534 RTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ-------TMVLRVTVGGSTTFDQGFPS 586

Db        497 RRNTFGDFVSLQVNINSPITQRYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQK 556

Qy        587 TMSANESLTSQSFRFAEFP-----------VGISASGSQTAGISISNNAGRQTFHFDKIE 635

Db        557 TMEIGENLTSRTFRYTDFSNPFSFRANPDIIGISEQPLFGAG-SISSG----ELYIDKIE 611

Qy        636 FIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDE 695

Db        612 IILADATFEAESDLERAQKAVNALFTSSNQIGLKTDVTDYHIDQVSNLVDCLSDEFCLDE 671

Qy        696 KRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSEN 755

Db        672 KRELSEKVKHAKRLSDERNLLQDPNFRGINRQPD-----------------RGWRGSTD 713

Qy        756 ITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYL 815

Db        714 ITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLKAYTRYELRGYIEDSQDLEIYL 773

Qy        816 IRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHS 875

Db        774 IRYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHHS 833

Qy        876 HHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKK 935

Db        834 HHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLLGEALARVKRAEKK 893

Qy        936 WRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLS 995

Db        894 WRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIAMIHAADKRVHRIREAYLP 953

Qy        996 ELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGHVDV-QQSHHR 1054

Db        954 ELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGLLCWNVKGHVDVEEQNNHR 1013

Qy       1055 SVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEE 1114

Db       1014 SVLVIPEWEAEVSQEVRVCPGRGYILRVTAYKEGYGEGCVTIHEIEDNTDELKFSNCVEE 1073

Qy       1115 EVYPTDTGTCNDYTA----HQGTAVCNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVR 1170

Db       1074 EVYPNNTVTCNNYTGTQEEYEGT--YTSRNQGYDEAYGNNPSVPADYASVYEEKSYTDGR 1131

Qy       1171 RDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228

Db       1132 RENPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1189
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RESULT 15
US-10-926-819-9
; Sequence 9, Application US/10926819
; Publication No. US20050049410A1
; GENERAL INFORMATION:
;  APPLICANT: Carozzi, Nadine
;  APPLICANT:  Hargiss, Tracy
;  APPLICANT:  Koziel, Michael G.
;  APPLICANT:  Duck, Nicholas B.
;  APPLICANT:  Carr, Brian
;  TITLE OF INVENTION: AXMI-003, A Delta-Endotoxin Gene and
;  TITLE OF INVENTION:  Methods for Its Use
;  FILE REFERENCE: 045600/281577
;  CURRENT APPLICATION NUMBER: US/10/926,819
;  CURRENT FILING DATE:  2004-08-26
;  PRIOR APPLICATION NUMBER: 60/498,518
;  PRIOR FILING DATE: 2003-08-28
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 1189
;   TYPE: PRT
;   ORGANISM: Bacillus thuringiensis
US-10-926-819-9

  Query Match             54.0%;  Score 3495.5;  DB 17;  Length 1189;
  Best Local Similarity   56.9%;  Pred. No. 6.9e-259;
  Matches  716;  Conservative  143;  Mismatches  290;  Indels  109;  Gaps   20;

Qy          7 NENEII--NALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAG 64

Db          5 NQNQCIPYNCLS------------NPEEVLLDGERISTGN--------SSIDISLSLVQ 43

Qy         65 RILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTALARL 124

Db         44 FLVSNF-VPGGGFLVGLIDFVWGIVGP---SQWDAFLVQIEQLINERIAEFARNAAIANL 99

Qy        125 QGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMV 184

Db        100 EGLGNNFNIYVEAFKEWEEDPNNPATRTRVIDRFRILDGLLERDIPSFRISGFEVPLLSV 159

Qy        185 YAQAANLHLLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRG 244

Db        160 YAQAANLHLAILRDSVIFGERWGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNNLPK 219

Qy        245 TNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMA 304

Db        220 STYQDWITYNRLRRDLTLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPL----INFN 275

Qy        305 SMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPI 364

Db        276 PQLQSVAQLPTFNVMESSAIRNPHLFDILNNLTIFTD---WFSVGRNFYWGGHRVISSLI 332

Qy        365 GGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLL----WGIYLEPIHGVPTVRFN 420

Db        333 GGGNITSPIYGREANQEPPRSFTFNGPVFRTLSNPTLRLLQQPWPAPPFNLRGVEGVEFS 392

Qy        421 FRNPQNTFE---RGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLIS 477

Db        393 --TPTNSFTYRGRGTV-------------DSLTELPPEDNSVPPREGYSHRLCHATFVQ 436

Qy        478 QSRVHV----PVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDII 533

Db        437 RSGTPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDIL 496

Qy        534 RTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ-------TMVLRVTVGGSTTFDQGFPS 586

Db        497 RRNTFGDFVSLQVNINSPITQRYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQK 556

Qy        587 TMSANESLTSQSFRFAEFP-----------VGISASGSQTAGISISNNAGRQTFHFDKIE 635
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Db        557 TMEIGENLTSRTFRYTDFSNPFSFRANPDIIGISEQPLFGAG-SISSG----ELYIDKIE 611

Qy        636 FIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDE 695
              |   |||||| ||||||:|||||||::|   |||||||||||||||| ||||||||||
Db        612 IILADATFEAESDLERAQKAVNALFTSSNQIGLKTDVTDYHIDQVSNLVDCLSDEFCLDE 671

Qy        696 KRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSEN 755
              |||| |||:|||||||||||||||  ||:|||                  || || :
Db        672 KRELSEKVKHAKRLSDERNLLQDPNFRGINRQPD-----------------RGWRGSTD 713

Qy        756 ITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYL 815
              |||| |:||||||||||||| :||||||||||| ||:|||||||:|||||||||||||||
Db        714 ITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLKAYTRYELRGYIEDSQDLEIYL 773

Qy        816 IRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHS 875
              |||||||| ::|||| |:|||| :||||:|||||||||| ||||||||||||||||||||
Db        774 IRYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHHS 833

Qy        876 HHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKK 935
              |||:||||:|||||:|:|||||:||||||:||||||||||:||||||||||:||||||||
Db        834 HHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLLGEALARVKRAEKK 893

Qy        936 WRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLS 995
              ||||||||||||  || ||||:||||||:|||:||| |||| ||||||| |||||||||
Db        894 WRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIAMIHAADKRVHRIREAYLP 953

Qy        996 ELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGHVDV-QQSHHR 1054
              |||||||||| |||||||| || ||||||||:||||||||| |||||||||| :|::||
Db        954 ELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGLLCWNVKGHVDVEEQNNHR 1013

Qy       1055 SVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEE 1114
              |||||||||||||| ||||||||||||||||||||||||||||:||||||| || ||
Db       1014 SVLVIPEWEAEVSQEVRVCPGRGYILRVTAYKEGYGEGCVTIHEIEDNTDELKFSNCVEE 1073

Qy       1115 EVYPTDTGTCNDYTA----HQGTAVCNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVR 1170
              |||| :| |||:||     ::||    ||| ||::||  : :   :|   |||::||| |
Db       1074 EVYPNNTVTCNNYTGTQEEYEGT--YTSRNQGYDEAYGNNPSVPADYASVYEEKSYTDGR 1131

Qy       1171 RDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
              |:| || :||| :| ||||||:||:||||||||||||||||| ||||||||||||
Db       1132 RENPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1189
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Search completed: May 24, 2005, 14:26:32
Job time : 197 secs